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ALIGNMENTS

JOURNAL REFERENCE AUTHORS TITLE KEYWORDS SOURCE RESULT 1
HSA295695
LOCUS
DEFINITION
ACCESSION REFERENCE VERSION JOURNAL TITLE AUTHORS ORGANISM Homo sapiens mRNA for stabilin-2 (STAB2 gene). AJ295695 AJ295695.1 GI:18073427 STAB2 gene; stabilin-2. Politz,O., Gratchev,A., McCourt,P.A.G., Schledzewski,K., Guillot,P., Johannson,S., Birk,R., Hakiy,N., Franke,P., Kodelja,V. Kannicht,C., Orfanos,C.E., Johannson,S. and Goerdt,S. Stabilin-1 and stabilin-2 constitute a novel family of fasciclin domain-containing adhesion molecules associated with endothelial-macrophage differentiation and angiogenic processes Gratchev,A.
Direct Submission
Submitted (27-JUL-2000) Gratchev A., Department of Dermatology, Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Unpublished Homo sapiens (sites) (bases 1 to 8266) Linear PRI 04-JAN-2002 Kodelja, V.,

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tacattattcattacaacctggcaagtgcaatcgagtctgcagatgcttatactgtgttc 120
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VYWSRCPANSEPTALFTHRCVYSGRFGSLKSGCARYCNATVKLIPKCKGFYGPDCNQC
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CNNRIDSDGACLTGTCRDGSAGRLCDKQTSACGPYVOFCHIHATCEYSNGTASCICKA
GYEGDGTLCSEMDPCTGITPGGCSRNAECIKTGTGTHTCVCQGGTGNGRDCSEINNC
LAPSAGGCHUNASCLYVGPGQNEDECKKGFRGNGIDCEPTTSCLEQTGKCHPLASCOS
TSSGVWSCVCQEGYEGDGFLCYGNAAVELSFLSEAAIFNRWINNASLQPTLSATSNLT
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2058 c 2111 g
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HGQCDDG1TGSGQCLCETGWTGPSCDTQAVLPAVCTPPCSAHATCKENNTCECNLDYE
GDG1TCTVVDFCKQDNGGCAKVARCSQKGTKVSCSCQKGYKGDGHSCTELDPCADGLN
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LLLENLKLISNATSLQGEPIYISYSQSTYYINNKAKIISSDIISTNGIYHIIDKLLSP
KNLLITPKDNSGRILQNLTTLATNNGYIKFSNLIQDSGLLSYITDPIHTPYTLFWPTD
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GNFLHLAKVDGNITIEGASIVDGDNAATNGVIHIINKVLVPQRRLTGSLPNLLMRLEQ
MPDYPIFRGYIIQYNLANAIEAADAYTVFAPNNNAIENVIREKKVLSLEEDVLRYHVV
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EHTFESNNEQTIMTMLQPRYSKFRSLLEETNLGHALDEDGVGGPYTIFVPNNEALNNM
KDGTLDYLLSPEGSRKLLELVRYHIVPFTQLEVATLISTPHIRSMANQLIQFNTTDNG
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NANCTTVAPGRTECICQKGYVGDGLTCYGNIMERLRELNTEPRGKWQGRLTSFISLLD
KAYAWPLSKLGPFTVLLPTDKGLKGFNVNELLVDNKAAQYFVKLHIIAGQMNIEYMNN
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GRWGPDCIECPGGAGSPCNGRGSCAEGMEGNGTCSCQEGFGGTACETCADDNLFGPSC
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LETGRVAYPTAFASQNCGSGVVGIVDYGPRPNKSEMMDVFCYRMKDVNCTCKVGYVGD
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CTLINVCLTKNGGCSEFAICNHTGQVERTCTCKPNYIGDGFTCRGSIYQELPKNPKTS
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KVLEIQKNRCDNNATTIIRGRCRTCSSELTCPFGTKSLGNEKRRCIYTSYFMGRRTLF
IGCQPKCVRTVITRECCAGFFGPQCQPCPGNAQNVCFGNGICLDGVNGTGVCECGEGF
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/protein_id="CAC82105.1"
/db_xref="GI:18073428"
/translation="MMLQHLVIFCLGLVVQNFCSPAETTGQARRCDRKSLLTIRTECR
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/db_xref="taxon:9606"
187. .7842
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NGTCHTSANCLTNSDGTASCKCAAGFQGNGT1CTAINACEISNGGCSAKADCKRTTPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           {\tt KCGAGRDIGDLFLNGQTCRIVQRELLFDLGVAYGIDCLLIDPTLGGRCDTFTTFDASG}
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79.1%;
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Pred. No. 0;
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1196	1137 cccqtgttttggagaaccatggtggctgtgacagaaatgcagagtgcacacagacag	Qy
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1136	gggtgtgtgtgtgcaaggcaggcta	Qy
1076 4670	1017 tgagaccagcaatggaggatgttctacaaaggccgactgtaaaagaaccaccccaggaaa 	Qy Db
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1016	caaatgtgcgg	Qy
4550	91 CTGCAATGGGACATGCCATACCAGCGCCCAACTGCACCAACTCAGATGGTACAGCT	Db .
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4490	837 ctgtgactgtgacgtcggctggcgaggagtgaagtgtgacatggagatcaccacagacaa	Qy Db
	ACCAAGCATGTTCTTGTGTCCATGGGAGATGCAACCAAGGACCCTTGGGAGATGGCTC	Db
836		Qy
4370	ACAGCCTGCGAGACCTGCACCGAGGGCAAGTACGGCATCCACTG	Db
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4310	TIGGTAATGGCATCTGT-TTGGATGGAGTGAATGGCACAGGTGTGTGAGTGTGG	DЬ
716	gctctgggaacggcttctgtctggacggtgtgaatggcactggcacgtgccagtgc	Qy
4251		Db
656	gctg-gctggcttctttggcccacaatgccaagcctgccccgggagaggtcaaaatgtg	Qγ
4191	CCTGTTTATTGGGTGCCAGCCAAAATGTGTGAGAACCGTCATTACGAGAGAA	dd
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537	agacaaaaccacttagagagacgaggaaatgcatctattccatctacttcatgggg	Оy
0	421 GCCACTACTATTATACGAGGAAGATGTAGGACATGCTCCAGAGGCTGACCTGCCCATTC	Db
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420	361 ggagtgatccatggtctggagaaagttctggaaattcaggaagaacagatgtgacaataat	24
3951	ATGACCAGCTCTATGTAAATGAGGCTCCAATAAACTACACCAATGTAGCCACTGATAAG	Db
360	301 aatgaccagctgtatgtaaatgaagctccaataaactacaccaatgtggccactgataaa	Qy
3891	CGTGAGACCATGCTGGGTTTCTCCTATTTCCTTAGCTTCTTCTCAT	Db
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2216 5810	157 aaacgaacaaatgtgcagattcatacaccggggactcttgtttgacgtgggtgtgggccta 2	Qy 2 Db 5
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2036	77 ggacttcctgttcaatcaagacaacaaggccaagctgaagtcttacctgaagttccacgt	у н
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20 6	57 gtcccaggttcttcgctatcacgtggtgggctgccagcagctgctgttggacaacctaaa	5 н
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1496 5090	37 gttgcaggagcatgctgtccgagagcttgctggacctggccccttcaccgtgttcgcgcc	Qy 1 Db 5
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GGG	CTATGCCCAGAAGGCCAAGTACCACCTGTGCTCAGCAGGCTGGCT	6888	Db
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GAGG 6587	GGGCACAGCTGCACAGAGATAGACCCCTGTGCAGACGGCCTTAACG	6528	Db
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ATGA 64	CTGC	6348	Db
acg	tyctccgtgcacgccacctgtacggagaacaacacgtgtgtgt	2757	Qy
1 CCTCC 6347		6288	Дb
ctg	ggtggacagccgcttcgtgtgacactcccacagctgtattcgcagtgtgcaca	2697	Qy
3AAAC 6287	CTCAGACCACGGACAGTGCGATGATGGCATCACGGGCTCCGGGCAGTGCCTCTGTG		Db
- a - a	cyaycatygacaytytyatgayyyyatcacayyotocyyyyaytycototyt	2637	Qу
GCT	GACGGCGTGTGAGATGTGCTGGCCCGGGAGATTTGGGCCTGATTGTCTGCCCTGTG	6168	Db
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acg	gtgccgcgatctgtacacacccatgggacagtgcctatgccacaccggcttc	2517	Оу
CGGGG 6107	CTTCGGGCGAGACTGTCAGGCCTGCCCTGGAGGACCAGATGCCCCCGTGTAATAACC	6048	DЪ
999	tcatgccagactgtcaggcctgcctggaggaccagatacaccgtgtaacaac	2457	Qy
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AC -		5931	рb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (24-AUG-2000) Osamu Ohara, Kazusa DNA Research Institute, Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp/NEDO, Tel:81-438-52-3913, Fax:81-438-52-3914)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5' - & 3'-end one pass sequencing and clone selection: Kazusa DNA Research Institute.

Location/Qualifiers
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Ohara,O., Nagase,T., Kikuno,R. and
The nucleotide sequence of a long
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/ LTAINS LATION - WHILFEWSDOTGVCECGEGFSGTACETCTECKYGIHCDQACSCVH
/ LTAINS LATION - WHILFEWSDOTGVCECGEGFSGTACETCTECKYGIHCDQACSCVH
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1 to 4575)
                                                                                                                                  LAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENETLSGRDIEHHLANVSMFFYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .4575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is not identified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Okumura, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Okumura, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone:as00112
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N	183 cytaggagtattccatctacyctccccactgggccagtacaaactgacatttgacaaag	Qy
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3122 3055	(63 ctatgtcggggacggagtgg 	рь
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2635	2576 CCACGGACATGATGGCATCACGGGCTCCGGGCAGTGCCTCTGTGAAACGGGGTG	D . 4
70	A3	Q !
2575	2083 - ماركومورتوركوموركوموركوموركوموركوموركومورك	Db dg
5	56 CCTTGATCAGTACTCGGCCACCGGAGAGTGTAAATGCAACACCGGCTTCAATGGGACG) B
58	2	Qy
2522 2455	2463 gccagactgtcaggcctgccctggaggaccagatacaccgtgtaacaaccggggcatgtg	ОУ
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- tcagaagaggacattgatgtcttggcttttggcaagcagcagccaagaa 	01	Фр
O t	95	Qy Db
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ccagaaggocaagtatcacctgtgctcggccggctggctggagagtgggcggggttg 	3301 3236	Qy Db
	3176	Db
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В δÃ DЬ δÃ В

SOURCE

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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tccacctcctctgagcctat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ggttaalctgggattgtcgccagggctaaggagccatgttgcctggatacctgggggacc 4435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTTCCTCCTCTGACCCTTT 4391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCTGATCTGGGGGGTTGTTCTGTGGGTGAGAGATGTGTTG-CTGTGCCCACCCAGTACA 4371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens mrNA; cDNA DKFZp434E0321 (from AL133021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone (DKFZp434E0321) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@frzpd.de Further information about the clone and the sevencing project is available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Martinsried, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Ca
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by LMU (Ludwig Maximilians University,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blum, H., Bauersachs, S., Mewes, Direct Submission Submitted (15-NOV-1999) MIPS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Munich/Germany) within the cDNA sequencing consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL133021.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.mips.biochem.mpg.de/proj/cDNA/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bauersachs, S., Mewes, H.W., Gassenhuber, J. and Wiemann,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 to 3642)
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TCTCCCAAAAATTTGCTTATCACTCCCAAAGACAACTCTGGAAGAATTCTGCAAAATCTT
                     gtcctgtccagtgacatcatcagcaccaatggcgtcatccacgttatagacaagttgctg
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	2964	Dy 2905 acccaagtctcttgcagctgcaagaaaggctacaagggggatggctacagctgcatagag	Qy
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	2844 1917	Qy 2785 aacaacacgtgtgtgtgtgtaacttgaactacgaaggtgacgggatcacatgcacagtcgtg	ā ö
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	2724 1797	Qy 2665 atcacaggctccggggagtgcctctgtgaaacagggtggacagccgcttcgtgtgacact	DP DP
- "	2664 1737	Dy 2605 agatttgggoctgactgtcagccccgcagctgctccgagcatggacagtgtgatgagggg 	Db Qy
	2604 1677	Dy 2545 ggacagtgcctatgccacaccggcttcaacgggacagcctgcgagctctgctggcatggg	Qy dd
	2544 1617	2485 ggaggaccagatacaccgtgtaacaaccggggcatgtgccgcgatctgtacacacccatg	дь 0у
	2484 1557	2425 gtgatccaaacccccaggtgctgccatggttacttcatgccagactgtcaggcctgccct	Оу
	2424 1497	2365 atotacaacccgttacctttcaggaggaacgtggaaggctgccagaacctgtgcaccgtg 	Qy Db
	2364 1440	2305 tgcattttcactcccaaatgcccactgaagagcaagccaaagggcgtgaagaagaagtgt 	Qy Db
	2304 1380	2245 accctaggtggccgatgtgacacttttactaccttcgatattccgggggggg	Qy Db
	2244 1320	2185 oggggactettgtttgaegtgggtgtgggeetatggeattgaetgeetaeteatgaateet 	Qy Db
	2184 1260	2125 ggaactggcagtgacatcggtgagctctttctaaacgaacaaatgtgcagattcatacac 	Oy Db
	2124 1200	2065 gacetececaggtetgetteetggaagaeeetgeaaggeteagagetgagtgtgaggtgt 	Db Qy
	2064 1140	2005 gacaagctgaagtcttacctgaagttccacgtgatccgagactccaaggctttagcttca 	ОУ
	200 4 1080	1945 aaagecetggaagecttgeeeceagageaggaetteetgtteaateaagaeaaeaag 	ОУ
	1944 1020	1885 ttgctgtcagtcatcactgactccatccaccccagtcactgtcttctggcctacggac	Оу
	960		Db

4041 3010	atattctgtgccgtcgtcctggtcactggtgcgattgctctggcagcttactcttacttc	3982 2951	Qy Db
3981 2950	gaacetttgagageteeteecaeggeageaggetgeeeaetetggeetgggaeaggt 	3922 2891	Qy Db
െ ശ	aatggaatcctccatattatttc AATGGGATCATTCATGTCATTTC	3862 2831	Qy Db
8 8	aagagaccaggtttgtgga CGGAGACCAGGTTTGTTGA	3805 2771	Qy Db
7	tctgaggactatgctgggaag	3745 2711	Qy Db
	tgagcacca :::::::::::::::::::::::::	3685 2651	Qy Db
3684 2650	tttttgaaacacctgactgacctgtccatccgtggcaccctgtttgtgccacagaacagt	3625 2591	Фу
3624 2590	tcctgacagaggtgctggctttttccaagagctcagcccgaggacaggca 	3565 2549	Qy dd
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3564	gggagatggcttctcgtgcagtgggaacctgctgcaggtcctcatgtccttcccctcg	3505	Qy
2548	atgtgggatgtottotgttaccggatgaaagatgtgaactgcacctgcaaggcaggc	3445 2518	ОУ
51	CTGTGGCTCTGGTGGGTTGGGATAGTGGACTATGGACCTAGACCCAACAAGAGTGAA	4.5	Db
3444	agtgtggtgcaaacgttgttgggatcgtagactacggatccagggccaacaagagtgaa	w	Qу
3384 2457	tgctcggccggctggctggagagtgggcgggttgcctacccgactacgtatgcctctcag	3325 2398	Оу
3324 2397	gctgcgaccatagccacctacaaccagctctcctatgcccagaaggccaagtatcacctg	3265 2338	Qy Db
3264 2337	tccccactgggccagtacaaactgacatttgacaaagccaaagaagcctgtgccaaagaa 	3205 2278	Qy Db
2 4	gatgcagctgtgcagacctctacttccaggacacgacgtaggagatattccatctacgc	3145 2218	Оу
20 1	tgagoctgagoagotgoogotogacogttgottacaggacaacggacagtgocaccoa	08	Qy Db
P 0	tcactatgtcggggacggagtggac 	30 2 5 2098	Qy Db
3024 2097	atagaccctgtgcagacggtgtcaacgggggatgccatgagcacgccacctgcaggatg:	2965 2038	Qy Db
03	CAGAAGGGATACAAAGGGGACGGGCACAGCTGCACAGAG	97	DЬ

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REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens CD44-like precursor FELL mRNA, complete cds. AF160476
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/db_xref="taxon:9606"
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                                           gggttctgcaaaatcttactacagtggcagcaaaccacggatataccaaattcagcaagt
                                                                         TCATAGACAAATTGCTATCTCCCAAAAATTTGCTTATCACTCCCAAAGACAACTCTGGAA
                                                                                   ttatagacaagttgctgtctcccaaaaacttgcttatcacccccaaagatgccttgggca
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Shimkets,R.A., Lichenstein,H., Vernet,C.,
Polypeptides and nucleic acids encoding
Patent: WO 0136638-A 11 25-MAY-2001,
Curagen Corporation (US)
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/db_xref="taxon:9606"
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                                 GATGCTCCCAGAAGGGCACGAAGGTCTCCTGCAGCTGCCAGAAGGGATACAAAGGGGACG
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Best Local Similarity 77.6%;
Matches 1524; Conservative
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                                  GGGTGTTCCATCTACGCTCCCCACTGGGCCAGTATAAGCTGACCTTTGACAAAGCCAGAG
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AGCTGAGTGTGAAATGTGGAGCTGGCAGGGACATCGGTGACCTCTTTCTGAATGGCCAAA
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97191544
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Submitted (27-AUG-1996). Osamu Ohara, Kazusa DNA Res
1532-3, Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913)
                                                                                                                                                                                                                                                                                                                                                                                  Ohara, O., Nagase, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                  Prediction of the coding sequences of unidentified human (The coding sequences of 80 new genes (KIAA0201-KIAA0280) (analysis of cDNA clones from cell line KG-1 and brain DNA Res. 3 (5), 321-329 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nagase, T., Seki, N., Ishikawa, K., Ohira, M., Kawa
Ohara, O., Tanaka, A., Kotani, H., Miyajima, N. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KIAA0246 protein; KIAA0246.

Homo sapiens male bone marrow myeloblast cell_line:KG-1 mRNA, clone_lib:pBluescript II SK clone:ha046061.
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1 (bases 1 to 6777)
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                                                 for KIAA0246 has a 1-bp deletion a
the sequence of KIAA0246"
/codon_start=2
/product=""""
                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/clone="ha046061"
/sex="mal-"
/product="KIAA0246 protein"
/protein_id="BAA13377.1"
/db_xref="GI:1665761"
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GRVFLQLRVAVAMMDQGCREILTTAGPFTVLVPSVSSFSSRTMNASLAQQLCRQHIIA
                                                                                                                                          /gene="KIAA0246"
<1. .>6637
                                                                                                                                                                                                /cell_line="KG-1"
/cell_type="myeloblast"
/tissue_type="bone marr
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                                                        gttctggaaattcagaagaacagatgtgacaataatgacaccattattgtgagagggag
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EGSIYLMDFARVYSSDHBAVNGILHFIDRVLLPPEALHWEDDDA,DIPRRNVTAAAQGF
GYKIFSGLLKVAGGLLPLLREASHFFTMLWFDDAAFRALPDRQAWLYHEDHRDKLAA
ILRGHMIRNVEALASDLPNLGPLRTMHGTPISFSCSRTRPGELMVGEDDARIVQRHLP
FEGGLAYGIDOLLEPPGLGARCDHFETRPLRLMTCSICGLEPPCPEGSQEGGSPBACW
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GLVAGALYLRARGKPMCFGFSAQAEDDADDDFSPWQEGTNPTLVSVPNPVFGSDTFC
EPFDDSLLEEDFPDTGRILTVK"
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LHFQERRAGVFHLQATSGPYGLNFSEAFACEAQGAVLASFPQLSAAQQLGFHLCLMG
MLANGSTAHPVYFPVADCGURRYGIVSLGARKNLSERWDAYCFRVQDVACRCRNGFVG
DGISTCNGKLLDVLAATANFSTFYGMLLGYANATQRGLDFLDFLDDELTYKTLEVPVN
EGFVUNMTLGGPDLELHASNATILSANASQGKLLPAHSGLSLLIISDAGPDNSSWAPVA
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CVNCTRRERCTOGFOLODTPRKSCVYRSGFSFSRCSVTYCAKKYPDCCPGFFCTLC
EPCPGGLGGVCSGHGOCODRFLKSGECHCHEGFHGTACEVCELGRYGPNCTGVCDCAH
GLCOEGLOGDCSCVCNVGWQGLRCDQKITSPOCPRKCDPNANCVODSAGASTCACAAG
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CQACPGGPSSPCSDRGVCMDGMSGSGQCLCRSGFAGTACELCAPGAFGPHCQACRCTV
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HHGGCHIHAECIPTGPQQVSCSCREGYSGDGIRTCELLDPCSKNNGGCSPYATCKSTG
DGQRTCTCDTAHTVGDGLTCRARVGLELLRDKHASFFSLRLLEYKELKDGPFTIFVP
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VFHVVTGLRWQAPSGTPGDPKRTIGQILASTEAFSRFETILENCGLPSILDGPGPFTV
FAPSNEAVDSLRDGRLIYLFTAGLSKLQELVRYHIYNHGQLTVEKLISKGRILTWANQ
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HARCVSQEGVARCRCLDGFEGDGFSCTPSNPCSHPDRGGCSENAECVPGSLGTHHCTC
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δÃ Db Qy 멍 Qy B δÃ В δδ Вр γQ В Qy Вр ρ В Qy Вb Qy Ър δÃ Вþ Qy Db δÃ д Qy Дb Qy В Qy Вþ δÃ DЬ Ş

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Hindenburgdamm 30, Berlin 12200,
                                                                                                                                                                                                                                                                                                                                                                                      Submitted (25-NOV-1999)
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nmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                GYWGSRCHECPGGAETPCNGHGTCLDGMDRNGTCVCQENFRGSACQECQDPNRFGPDC
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31. .7743
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                                                                                                                                                                              /gene="stab1"
                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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BASE COUNT ORIGIN Query Match Best Local : 14.8%; 51.5%; Pred. No. 6.9e-188; 9; Length 7870;

Local Similarity

Pred.

Db Q Matches 2066; 3433 CTGGACTTGGTGCCTTCCAGCCTCTTCCGGGAATTGCTGCAGCACCATGGGTTGGTG 25 ctggagcagatgcccgactattccattttccgaggttacattattcattactaccatggca Conservative 0; Mismatches 1823; Indels 125; Gaps 3492 84 15;

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145 aactatatcagggagaagaaagccacatctctaaaggaagatattctacggtaccatgtg CCCCAGATTGAGGCTGCCACTGCCTACACCATCTTTGTGCCCACCAACCGCTCCCTGGAG 3552 204

DЪ Qy GTCCTGGGGGAGGCCCTCTCCATGGAAACCCTGCGGAAGGGTGGACACCGCAACTCCCTC gtcctgggggaaaagctcctgaagaatgacttgcataacggcatgcaccgagagaccatg 264

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Patent WO0136638.
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                                                                                                                                                                                                                                                                               Score 637.6; DB 6;
Pred. No. 7.2e-171;
0; Mismatches 224;
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REFERENCE
AUTHORS
TITLE
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SOURCE
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AX149463
             FEATURES
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Sequence 19
AX149463
AX149463.1
                    Bukaryota; Metazoa; Chordata; Craniata; Mammalla; Eutheria; Primates; Catarrhini 1 (bases 1 to 1577)
Shimkets,R.A., Lichenstein,H., Vernet,C. Polypeptides and nucleic acids encoding patent; Wo 0136638-A 19 25-MAY-2001; Curagen Corporation (US)
                                                                                                   Homo sapiens
Location/Qualifiers
1. .1577
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                                                                                                                                     GI:14347937
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WO0136638.
                                                                              Craniata; Vertebrata; Catarrhini; Hominidae
                                                       Vernet, C.
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617; Conservative
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AC025501
Mus musculus
SEQUENCE, 18
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/db_xref="taxon:9606"
410 c 342 g 40
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78.8%;
            chromosome
unordered |
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Pred. No. 2e-136;
0; Mismatches 16
                      218073 bp
me 10 clone
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (09-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 25, 2001 this sequence version replaced gi:8077096. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J. Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N., O'Neil,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
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Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
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Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 218073)
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                      as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                           Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 213014 bases at least Q40
Consensus quality: 214764 bases at least Q30
Consensus quality: 215528 bases at least Q20
                                                                                                                                                                                                                                                                                                                 Insert size: 210000: agarose-fp
Insert size: 216373: sum-of-contigs
Quality coverage: 10.2 in Q20 bases; agarose-fp
Quality coverage: 9.9 in Q20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: L8063
Center clone name: 129_O_23
Center clone name: 129_O_23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
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                  23322 23421: gap of 100 bp in length 23422 24539 contig of 1108 bp in length 24530 24629: gap of 100 bp 26630 26959: contig of 2330 bp in length 24530 24629 gap of 2330 bp in length 24630 26959: contig of 2330 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Zainoun,J., Zimmer,A. and Zody,M.
27059: gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Castle, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barna, N., Bastien, V., Beda, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ., Lander, E., Abraham, H., Allen, N.,
                                                                                                               in length
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208798 218073: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43366 43465: gap of 100 bp
43466 46874: contig of 3409 bp in
46875 46974: gap of 100 bp
46975 51691: contig of 4717 bp in
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43366 43465:
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28341. .30420
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30521. 32131
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133851. .151236
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/clone_lib="RPCI-23 Female
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43365: contig of
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40349: contig of 3533 l
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36716: contig of
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340: gap of 100 bp
30420: contig of 2080 bp
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RESULT 15
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Best Local Similarity
Matches 166; Conserv
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              Burch, Bireva, Birwi, B. Dirwi, M. Byrdn, N. F., Burch, P. Burch, B. Burch, B. Burch, B. Burch, B. Burch, Chen, G., Chen, G., Chen, G., Chen, G., Chen, E., Chen, E., Cheokhay, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y. Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Heward, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Lawis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Martinez, E., Massey, E., Mahniney, E., McLeod, M.P., Meador, M., Mayuan, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mahniney, E., McLeod, M.P., Meador, N., Ngyen, N., Ngyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuon, G., Oragunye, N., Oviedo, R., Payton, B., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Rolfe, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 157216)
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/note="assembly_fragment
   Ren,Y., Rives,M., l
avery,G., Scherer,S
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Pred. No. 4.6e-32;
0; Mismatches 20;
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ne 3 clone RP11-54J3,
Rojas, A., F
S., Scott, G
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   Shen, H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (28-JAN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Oct 14, 2001 this sequence version replaced gi:12043785.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct
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Chemistry: Dye-primer Bodipy: 15% of reads chemistry: Dye-terminator Big Dye: 85% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 150347 bases at least Q40 Consensus quality: 159720 bases at least Q30 Consensus quality: 182034 bases at least Q30 Consensus quality: 182034 bases at least Q30 Consensus quality: 175036; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 2.5x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                  Center clone name: RP11-54J3
                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: HACM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Project Information
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               estimation
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* NOTE: Estimated insert size may differ from sequence length arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 33 contigs. The true order of the pieces
is not known and their order in this sequence record is be preserved as soon as it is available and the accession number will 71247 71347 715527 75627 79096 79196 83354 83454 87769 64197 64297 59053 58953 52673 52773 47023 47123 30847 22905 23005 30747 $14173 \\ 14273$ 39032 38932 75626: 79095: 5905 3893 14272: gap of 22904: contig 471 64196 30746: gap c gap of gap of contig gap of conti contig gap o gap o gap o conti gap o gap o gap o gap o contig of 14172 bp in length contig f unknown length g of 8632 bp in f unknown length g of 7742 bp in unknown of 6180 unknown of 5144 unknown of 7991 unknown of 8085 unknown of 4315 unknown of 4158 unknown of 3469 unknown of 4180 unknown of 6950 of 5550 unknown length bp in length bp in l length bp in l bp in length length length bp in l nt dq dq length bp in bp in length bp in length nr dq length length length length length in length length

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Best Local Similarity
Matches 166; Conserv
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                                                                                                                                                                 AGAAGGGCACGAAGGTCTCCTGCAGCTGCCAGAAGGGATACAAAGGGGACGGGCACAGCT 114050
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/db_xref="taxon:9606"
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1. 157216
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Pred. No. 5.1e-30;
0; Mismatches 32;
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AAS28848	ABA06754	AAS28787	ABA06583	AAA61263	AAK30592	AAH78221	AA167200	AAS92463	AAQ03324	AAK52641	ABA09190	AAK51657	AAH28219	AAV43590	AAS92464	ABA83182	AAA39054	ABA08712	AAF72410	AAS45938	AAX52252	AAI58121	AAA57364	AAD08974	AAH23114	AAS84364	AAD06019	AAV71778	AAQ27190	AAS62772	AAS00854	AAA57363	AAF87121	AAF87118	AAC76373
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ALIGNMENTS

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ABA04648
                                                                                                                               RESULT
Rat Hyaluronic Acid Receptor for Endocytosis, HARE, coding sequence
                                22-FEB-2002
                                                                ABA04648;
                                                                                               ABA04648 standard; cDNA;
                              (first entry)
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                                                                                                ВP
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HARE; Hyaluronic Acid Receptor for Endocytosis; hyaluronan; chondroitin; chondroitin sulphate; extracellular matrix; cartilage; skin; vitreous humour; endocytic receptor; glycosaminoglycan; rat;

Rattus norvegicus.

25-APR-2000; 02-NOV-2000; CDS 25-APR-2001; WO200181544 - A2 2000US-199538P 2000US-245320P 2001WO-US13403 /partial /note= /*tag= 1..4296 Location/Qualifiers /product= "Rat HARE" "No start codon given' D

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160	ggctgccagaacctgtgcaccgtggtgatccaaacccccaggtgctgccatggttacttc 24	2401	Оβ
	caaagggcgtgaagaagagtgtatctacaacccgttacctttcaggaggaacgtg	34	Db
100	ggcgtgaagaagtgtatctacaacccgttacctttcaggaggaacgtgga	2341	Qy
340	ttttcactcccaaatgo	2281 2281	dq Vy
	atgaatcctaccctaggtggccgatgtgacacttttactaccttc 2	22	Db
	traactgootactcatgaatcotaccotaggtggcogatgtgacacttttactaccttc 2	2221	Qγ
220 220	atacaccggggactcttgtttgacgtgggtgtgggcctatggc 2 	2161 2161	Оy
160	tgaggtgtggaactggcagtgacatcggtgagctctttctaaac 2	2101	DЬ
160	yctcagagctgagtgtgaggtgtggaactggcagtgacatcggtgagctctttctaa	2101	Qy
100	ttcagacctccccaggtctgcttcctggaagaccctgca	2041	рb
040	.tcttgttcaatcaagacaacaaggacaagctgaagtottacctgaagttccacgtgatc 2	98	Дb
040	tcctgttcaatcaagacaacaaggacaagctgaagtcttacctgaagttccacgtgatc 2	1981	Qy
		1921	Db
980	tcactgtcttctggcctacggacaaagccctggaagccttgcccccagagcagcaggac 1	1921	Qy
920	agcaagttgatacaggactcaggcttgctgtcagtcatcactgactccatcca	98	Db 5
) (20	0
860 860		1801	Оу
800	tccaegttatagacaagttgctgtctcccaaaaacttgcttatcacccccaaagatgc	74	Db
800		4	Qy
740	ac	1681	Db

90	caagagaccaggtttgtggatggaagatccattctgcagtgggacatcatcgccgccaat	84	Db
3900		ρ α	0 5
3840	tttctgaggactatgctgggaagccaactgctcattaccttcagccaggaccagctccac	J 7	D Qy
3780	artgagcaccacctcactartgtcaacgtctccttttacaartgaccttgtcaarggtaccattgagcaccacctcactartgtcaacgtctccttttacaartgaccttgtcaatggtacc	3721	dd Vy
172	cctgtttgtgcacagaacagtgggctaccgggaaataagagcctgtctggccggga	_ O	Db
	ccctgtttgtgccacagaacagtgggctaccgggaaataagagcctgtctggccggga	CD.	Qy
3660	agagetcagecegaggacaggeatttttgaaacacetgacetg	3601	Db
	agagctcagcccgaggacaggcatttttgaaacacctgactga	~	Qy
6		(D	Db
3600	${\tt aggtcotcatgtccttcccctcgctcacaaacttcctgacagaggtgctggctttttc}$	(D	Оу
3540	actgcacctgcaaggcaggctatgtgggagatggc	4	Db
	actgcacctgcaaggcaggctatgtggggagatggcttctcgtgcagtgggaacctgct	4	Qy
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3420	acccgactacgta	1.1	Db
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ŵ	gcccagaaggccaagtatcacctgtgctcggccggctggct	w	Db
	cccagaaggccaagtatcacctgtgctcggccggcttggctggagagtgggcgggttgc	30	Qy
30		N	Db
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3240	ccgtaggagtattccatctacgctccccactgggccagtacaaactgacatttgacaa	₩.	Db
3240	ccgtaggagtattccatctacgctccccactgggccagtacaaactgacatttgacaa	3181	Qy
3180	caggacaacggacagtgccacccagatgccagctgtgcagacctctacttccaggacacg	₩.	Db
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3120	actatgtcggggacggagtggactgtgagcctgagcagctgccgctcgaccgttgctt	0	Qy
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3060	tyaycacyccacctycayyatyacyyycccayycaaycataaytytyaatytaaaay	3001	Qу
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3000	gggatggctacagctgcatagagatagacccctgtgcagacggtgtcaacggggggatg	2941	40
2940	gtcgctaagtgctcccagaaaggcacccaagtctcttgcagctgcaagaaaggctacaag	œ	Db
2940	togotaagtgotoccagaaaggoacccaagtotottgcagotgcaagaaaggotacaa	2881	Qy
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RESULT
ABA0467
ID ABA0
XX ABA0
XX ABA0
XX ABA0
DT 22-F
XXX
DE Huma
XXX
DE Huma
XXX Chon
KW Chon
XX Vitr
XX
OS Homo
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                                 HARE; Hyaluronic Acid Receptor for Endocytosis; hyaluronan; chondroitin sulphate; extracellular matrix; cartilage; skin, vitreous humour; endocytic receptor; glycosaminoglycan; hum
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                                                                                    Hyaluronic
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                                                                                     Acid
                                                                                                                                                              cDNA;
                                                                                    Receptor
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                                                                                     Endocytosis,
                                                  skin;
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QΥ
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                                                                                                                                                                                                                                                          Query Match 60.3
Best Local Similarity 79.3
Matches 3483; Conservative
                                                                                                                                                                                                                                                                                                                                   The present invention relates to sequences for rat and human HARE (Hyaluronic Acid Receptor for Endocytosis, ABA04648, ABA04652, AAM47675 and AAM47684). HARE can bind specifically to at least one of hyaluronic acid (HA, also known as hyaluronan), chondroitin (C) or chondroitin sulphate (CS). HA is an extracellular matrix component of all tissues, in particular cartilage, skin and vitreous humour. HARE is the endocytic receptor responsible for removing HA and other glycosaminoglycans from the circulation. The present sequence is the coding sequence for human table.
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nucleic acid
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02-NOV-2000;
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                                                                                                                                                                                                                                                                                                           Sequence
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 427
                    301
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DB; AAM47684.
                  attctacggtaccatgtggtcctgggggaaaagctcctgaagaatgacttgcataacggc
                                                                                                                                                                                      aacaatgaagccatcgaaaactatatcagggagaagaaagccacatctctaaaggaagat 186
attattgtgagaggggagtgtggaaagtgttcccagcaagccccctgcccactcgagaca
                                                                 cagctgtatgtaaatgaagctccaataaactacaccaatgtggccactgataaaggagtg
                                                                                               gtcctccggtatcatgtggtcctggaggagaaactcctgaagaatgacctgcacaatggc
                                                                                                                                                                            aacaacaatgccatcgagaattacatcagggagaagaaagtcttgtctctagaggaggac
                                                         cagctctatgtaaatgaggctccaataaactacaccaatgtagccactgataagggagtg
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2000US-245320P
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Wo start
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Pred. No. 0;
0; Mismatches
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240

426

180

Qy

2642	tgcgagctctgctggcatgggagatttgggcctgactgtcagccc	2583	Qy
2576		2517	Db
	gcgatctgtacacacccatgggacagtgcctatgccacaccggcttcaacgggaca	2523	Qy
		2457	Db
	ccagactgtcaggcctgccctggaggaccagatacaccgtgtaacaaccggggcatg 	ω 4	Qy Db
2462	gccagaacctgtgcaccgtggtgatccaaacccccaggtgctgccatggttacttca	ω 4	Qy
2396			Db
	aagggcgtgaagaagtgtatctacaacccgttacctttcaggaggaacgtgga 	ν ω	Оy
2342	ttccgggggagtgcggaagttgcattttcactcccaaatgcccactgaagagcaagc	2283	Qy
2279		2220	Db
⊢ ⊗	actgcctactcatgaatcctaccctaggtggccgatgtgacacttttactaccttcg	22	Qy
		16	Db
2222	caaatgtgcagattcatacaccggggactcttgtttgacgtgggtgtggcctatggc		Qy
2159			Db
2162	<pre>ctcagagctgagtgtgaggtgtggaactggcagtgacatcggtgagctctttctaaac</pre>	10	Qy
2099			Db
2102	agactccaaggctttagcttcagacctccccaggtctgcttcctggaagaccctgca	98	Qy
2039			Db
H 2	caatcaagacaacaaggacaagctgaagtcttacctgaagttcoacgtga	98	Qy
		92	Db
19	actgtcttctggcctacggacaaagccctggaagccttgccccagagcagcagg	8 9	Qy
19			Db
19 18	aagttgatacaggactcaggcttgctgtcagtcatcactgactccatcca	9.6	Qy Db
18	ggcagggttctgcaaaatcttactacagtggcagcaaaccacggatataccaaat	80	Qy
17		74	Db
180	ccacgttatagacaagttgctgtctcccaaaaacttgcttatcacccccaaagatg	6	Qy
173			Db
	gttcataaacaatgaggcgaaggtcctgtccagtgacatcatcagcaccaatggcgt	1683 1620	Qy Db
16	cacaagtgocacgaccotocaaggagagccagtttccatctctgtctctcaggaca	56	Qy
16		56	Db
1622	gttcttcgctatcacgtggtgggctgccagcagctgctgttggacaacctaaaagtga 	50	Qу
49	tgcagcctttgatgaggaagctcgggttaaagactgggacaaatacggtttaatgcccc	44	Db

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AAF87120 26-MAR-2002 coding standard; DNA; sequence (first entry)

3625 ВP

ARESULT AAF87120 JD AAF88 AC AAF88 XX AAF8 XX AAF8 XX NOV; KW CATC KW SETI KW SETI KW LOATC K NOV: Cytostatic; contraceptive; antiinflammatory; immunomodulatory; cardiovascular; casein kinase II phosphorylation site; contraception; serine/threonine kinase; Peutz-Jeghers syndrome; cellular proliferation; epidermal growth factor; cell development; apoptosis; cell adhesion; growth migration; cell structure; motility; cancer; immune disorder; inflammatory disorder; cellular adhesion disorder; long-QT syndrome; cardiovascular disease; hypertrophic cardiomyopathy; marfan syndrome; therapy; NOV1; NOV2; NOV3; NOV4; NOV5; NOV6; NOV7; NOV8; NOV9; NOV10; NOV11; NOV12; NOV13; NOV14; NOV15; NOV16; ds.

Unidentified

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                                                                                                                                                           the MOVI-NOVI6 proteins, and their coding sequences. The proteins have CC Cytostatic; contraceptive; antiinflammatory; immunomodulatory; and CC cardiovascular activities. The sequences may be used in the prevention, CC diagnosis and treatment of diseases associated with inappropriate NOVX CC expression. They may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of protein by expressing inactive proteins or to CC produce NOVX proteins, by inserting the nucleic acid into a cell and CC culturing it to express the protein. The DNA may be used as DNA probes in CC assays to detect and quantitate the presence of similar DNAs in samples, CC and which patients may need restorative therapy. The NOVX protein may CC also be used as antigens in the production of antibodies (Abs) against CC NOVX and in assays to identify modulators of NOVX expression and CC activity. The anti-NOVX Abs and antagonist are used to down regulate CC expression and activity. The anti-NOVX abs are used for detecting the CC presence of NOVX is samples. Disorders that may be prevented, diagnosed and/or treated vary depending on the NOVX protein NOVI, NOVS, NOVS, NOVS, NOVS, NOVS, Treated disorders (e.g. Peutz-Jeghers syndrome, cellular CC the epidermal growth factor (EGS) like super family and are involved in, CC e.g. regulation of cell development. Apontosis, cell adhesion of cell development.
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Best Local Similarity
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08-MAR-2000;
16-NOV-2000;
                                                                                                                                                                                          e.g. regulation of cell development, apoptosis, cell adhesion, growth migration, cell structure and motility and protein management, and are used to treat cancers, inflammatory disorders, immune disorders and cellular adhesion disorders. NOV6-10 are homologous to EGF-like fibrillin proteins and are used to treat cardiovascular disease e.g. hypertrophic cardiomyopathy, long-QT syndrome and marfan syndrome.
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                                                                                                                                                                                                                      This sequence encodes the NOVB protein. The invention relates to CC the NOV1-NOV16 proteins, and their coding sequences. The proteins have CC Cytostatic; contraceptive; antiinflammatory; immunomodulatory; and CC cardiovascular activities. The sequences may be used in the prevention, CC diagnosis and treatment of diseases associated with inappropriate NOVX CC expression. They may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC supplement the patients own production of protein. They are used to CC produce NOVX proteins, by inserting the nucleic acid into a cell and CC culturing it to express the protein. The DNA may be used as DNA probes in assays to detect and quantitate the presence of similar DNAs in samples, CC and which patients may need restorative therapy. The NOVX protein may CC NOVX and in assays to identify modulators of NOVX expression and activity. The anti-NOVX Abs are used for detecting the cexpression and activity. The anti-NOVX Abs are used for detecting the CC presence of NOVX in samples. Disorders that may be prevented, diagnosed CC NOV7, NOV9-11 and NOV13-16 have casein kinase II phosphorylation sites C characteristic of serincy/threonine kinases, and are used to treat the epidermal growth factor (EG)-like super family and are involved in, cell are cell development, apoptosis, cell adhesion, growth cc cellular adhesion disorders (NOY6-10 are homologous to FGF-11ke) and contents on the cell development, apoptosis, cell adhesion, and are used to treat the epidermal growth factor (EG)-like and notility and protein management; and are used to treat and contents in flammatory disorders, immune disorders and cc cellular adhesion disorders (NOY6-10 are homologous to FGF-11ke).
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                                                                                                                                  cardiovascular disease; hypertrophic cardiomyopathy; marfan therapy; NOV1; NOV2; NOV3; NOV4; NOV5; NOV6; NOV7; NOV8; NOV11; NOV11; NOV13; NOV14; NOV15; NOV16; ds.
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This sequence encodes the NOV6 protein. The invention relates to the NOV1 NOV16 proteins, and their coding sequences. The proteins have Cytostatic; contraceptive; and their coding sequences. The proteins have Cytostatic; contraceptive; and triangle sequences may be used in the prevention, Cd diagnosis and treatment of diseases associated with inappropriate NOVX CC expression. They may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of protein by expressing inactive proteins or to csupplement the patients own production of protein. They are used to CC supplement the patients own production of protein. They are used to CC supplement the express the protein. The DNA may be used as DNA probes in assays to detect and quantitate the presence of similar DNAs in samples, CC and which patients may need restorative therapy. The NOVX protein may call on the protein of antibodies (Abs) against CC NOVX and in assays to identify modulators of NOVX expression and activity. The anti-NOVX Abs and antagonist are used to down regulate considered vary depending on the NOVX protein. NOV1, NOV3, NOV5.

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CC expression. They may be used to treat disorders associated with decreased cc expression. They may be used to treat disorders associated with decreased cc expression by rectifying mutations or deletions in a patient's genome cc that affect the activity of protein by expressing inactive proteins or to cc supplement the patients own production of protein. They are used to cc produce NOVX proteins, by inserting the nucleic acid into a cell and cc culturing it to express the protein. The DNA may be used as DNA probes in casays to detect and quantitate the presence of similar DNAs in samples, cc and which patients may need restorative therapy. The NOVX protein may cc also be used as antigens in the production of antibodies (Abs) against CC NOVX and in assays to identify modulators of NOVX expression and cc expression and activity. The anti-NOVX Abs are used to down regulate cc presence of NOVX in samples. Disorders that may be prevented, diagnosed and/or treated vary depending on the NOVX protein. NOV1, NOV3, NOV5.

CC NOV7, NOV9-11 and NOV13-16 have casein kinase II phosphorylation sites characteristic of serine/threonine kinases, and are used to treat cc kinase related disorders (e.g. Peutz-Jeghers syndrome, cellular cc the epidermal growth factor (EGF) like super family and are involved in, cell development, apoptosis, cell adhesion, growth cc used to treat cancers, inflammatory disorders, immune disorders and cc cellular adhesion disorders. NOV5-10 are homologous to EGF-like cc fibrillin proteins and are used to treat cardiomyopathy, long-OT syndrome and marfan syndrome.
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29-NOV-1999;
08-MAR-2000;
16-NOV-2000;
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Cytostatic; contraceptive; antiinflammatory; immunomodulatory; and cried contraceptive; antiinflammatory; immunomodulatory; and city interest contraceptive; antiinflammatory; immunomodulatory; and contraceptive; antivities. The sequences may be used in the prevention, contraceptive; and contraceptive; and contraceptive; immunomodulatory; and contraceptive; and contraceptive; immunomodulatory; and contraceptive protein of protein sin a patient's genome contraception. They may be used to treat disorders associated with decreased expression. They are used to the patients of production of protein in a patient's genome contraception by rectifying mutations or deletions in a patient's genome contraception. They are used to contraception by inserting the nucleic acid into a cell and contraception, and protein may be used as DNA probes in the production of protein. They are used to casany to detect and quantitate the presence of similar DNAs in samples, and which patients may need restorative therapy. The NOVX protein may contraception and activity. The anti-NOVX Abs are used to down regulate expression and activity. The anti-NOVX Abs are used to down regulate contraception and activity. The anti-NOVX Abs are used for detecting the presence of NOVX in Samples. Disorders that may be prevented, diagnosed and/or treated vary depending on the NOVX protein. NOV1, NOV5, N
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29-NOV-1999;
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16-NOV-2000;
     Sequence
                                                                                                                                               used to treat cancers, inflammatory disorders, immune disorders and cellular adhesion disorders. NOV6-10 are homologous to EGF-like fibrillin proteins and are used to treat cardiovascular disease e.g
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/transl_except= (pos: 478..480, aa: Xaa)
/transl_except= (pos: 667..669, aa: Xaa)
/transl_except= (pos: 1105..1107, aa: Xaa)
/transl_except= (pos: 1138..1140, aa: Xaa)
/transl_except= (pos: 1158..1158, aa: Xaa)
/transl_except= (pos: 1168..1170, aa: Xaa)
/transl_except= (pos: 1171..1173, aa: Xaa)
/transl_except= (pos: 1249..1251, aa: Xaa)
/transl_except= (pos: 1249..1251, aa: Xaa)
/note= "Xaa is an unspecified amino acid; no
termination codon given"
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The present sequence encod specification describes for WF-HABP, WF-HABP, OE-HABP, for treating discorr

equence encodes a hyaluronan-binding protein. The describes four hyaluronan-binding protein, known as ABP, OE-HABP, and BM-HABP. The polypeptides are useful diseases such as proliferative conditions, metastasis,

proliferative

HABP, OE-HABP, and diseases such as p

Claim metastasis,

2;

Fig

4A-B;

457pp;

English.

hyaluronan-binding proteins, known as full-length WF-HABP, WF-HABP and BM-HABP, useful for treating proliferative conditions, astasis, inflammation, ischemia, arthritis and multiple scleros

sclerosis

WF-HABP

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Best Local Sim
Matches 1026;
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                                                                                                          AAY93910
                                                                                                                                                                   HUMAN GENOME
AMERICAN NAT
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ence dysfunction; immune surveillance dysfunction;
sclerosis; autoimmunity; immune dysfunction; alle
                                                                                                                                             GA,
                                                          BM-HABP, useful for treating proliferative conditions inflammation, ischemia, arthritis and multiple sclero:
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                                                                                                                                                                                                                               99WO-US30462
                                                                                                                                                                                                                                                                                                   /product= "hyaluronan-binding protein" /transl_except= (pos: 6341..6343, aa: Xaa) /transl_except= (pos: 6494..6496, aa: Xaa) /transl_except= (pos: 6536..6538, aa: Xaa) /note= "Xaa is an unspecified amino acid"
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                                                                                  as full-length WF-HABP, WF-HABP,
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The present sequence encodes a hyaluronan-binding protein. specification describes four hyaluronan-binding protein, k

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Fig

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English

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Matches 2065; Conserv
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RESULT 1
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AAC76373 standard; CDNA; 1377 ВΡ

08-FEB-2001 (first entry)

Human ORFX ORF1928 polynucleotide sequence SEQ ID NO:3855

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CC which represent the human ORFX open reading frames 1 to 3161. The ORFX CC sequences have activities such as: cytostatic; hepatotropic; vulnerary; CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective; CC antipsoriatic; anticonvulsant; antiarthritic; immunosuppression; CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; CC antidiabetic; hypotensive; dermatological; immunosuppressive; CC antidiabetic; hypotensive; dermatological; immunosuppressive; CC antidiabetic; hypotensive; dermatological; antinunosuppressive; CC antidiabetic; hypotensive; dermatological; immunosuppressive; CC antidiptical; and antiparamic. The sequences can be used for determining CC the presence of or predisposition to, or preventing or treating CC pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy CC vectors. The proteins and nucleic acids may be used to treat cancers, CC graft vs host disease, cardiovascular disease, diabetes mellitus, the proteins of 
                                                                                                                                                            Query Match
Best Local Similarity
Matches 900; Conser
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02-APR-1999;
05-APR-1999;
30-MAR-2000;
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08-MAR-2000;
16-NOV-2000;
           Cytostatic; contraceptive; antiinflammatory; immunomodulatory; and cardiovascular activities. The sequences may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate NOVX expression. They may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of protein by expressing inactive proteins or to supplement the patients own production of protein. They are used to produce NOVX proteins, by inserting the nucleic acid into a cell and culturing it to express the protein. The DNA may be used as DNA probes in assays to detect and quantitate the presence of similar DNAs in samples,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           growth migration; cell structure; motility; cancer; immune disorder; inflammatory disorder; cellular adhesion disorder; long-QT syndrome; cardiovascular disease; hypertrophic cardiomyopathy; marfan syndrome; therapy; NOV1; NOV2; NOV3; NOV4; NOV5; NOV6; NOV7; NOV8; NOV9; NOV10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cardiovascular; casein kinase II phosphorylation site; contraception; serine/threonine kinase; Peutz-Jeghers syndrome; cellular proliferation; epidermal growth factor; cell development; apoptosis; cell adhesion;
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                                                                                                                                                                                          This sequence encodes the NOV7 protein.
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                                                                                                                                                                                                                                                                       human polypeptides and the nucleic acids that encode them useful reventing, diagnosing and treating e.g. cancer, inflammation and
                                                                                                                                                                                                                                                           disorders
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patients may need restorative therapy. The NOVX protein may
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99US-167785P.
2000US-187844P.
2000US-0715417.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1508
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WPI; 200
P-PSDB;
                                                                                             19-NOV-1999;
29-NOV-1999;
08-MAR-2000;
16-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                             NOV: Cytostatic; contraceptive; antiinflammatory; immunomodulatory; cardiovascular; casein kinase II phosphorylation site; contraception; serine/threonine kinase; Peutz-Jeghers syndrome; cellular proliferation; epidermal growth factor; cell development; apoptosis; cell adhesion; growth migration; cell structure; motility; cancer; immune disorder; inflammatory disorder; cellular adhesion disorder; long-QT syndrome; cardiovascular disease; hypertrophic cardiomyopathy; marfan syndrome; therapy; NOVI; NOV3; NOV4; NOV5; NOV6; NOV7; NOV8; NOV9; NOV10; NOV11, NOV12, NOV3; NOV4; NOV5; NOV6; NOV7; NOV8; NOV9; NOV10;
                                        Shimkets RA,
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2001-648134/74
DB; AAB83366.
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ce expression by rectifying mutations or deletions in a patient's genome content the activity of protein by expressing inactive proteins or to content the patients own production of protein. They are used to content the patients own production of protein. They are used to content the patients own production of protein. They are used to content the protein activity are used to content the protein activity are used to continue Novy proteins, by inserting the nucleic acid into a cell and continue to express the protein. The DNA may be used as DNA probes in cassays to detect and quantitate the presence of similar DNAs in samples, and which patients may need restorative therapy. The NOVA protein may call and which patients may need restorative therapy. The NOVA sprotein may call into the production of antibodies (Abs) against convariant to identify modulators of NOVX expression and activity. The anti-NOVA Abs are used to down regulate correspond to and activity. The anti-NOVA Abs are used for detecting the correspond for detecting the correspond for treated vary depending on the NOVA protein. NOVI, NOV3, NOV5, Correspond to treated vary depending on the NOVA protein. NOVI, NOV3, NOV5, Correspond to treated vary depending on the NOVA protein. NOVI, NOV3, NOV5, Correspond to treated vary depending on the NOVA protein. NOVI, NOV3, NOV5, Correspond to treated vary depending on the NOVA protein. NOVI, NOV3, NOV5, Correspond to treat concers, inflammatory disorders, and are used to treat concers, inflammatory disorders, immune disorders and correspond to treat cancers, inflammatory disorders, immune disorders and correspond to treat cardiovascular disease e.g. the proteins and are used to treat cardiovascular disease e.g. the proteins and are used to treat cardiovascular disease e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence encodes the NOV10 protein. The invention relates to the NOV1-NOV16 proteins, and their coding sequences. The proteins have Cytostatic; contraceptive; antiinflammatory; immunomodulatory; and cardiovascular activities. The sequences may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate NOVX expression. They may be used to treat disorders associated with decreased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human polypeptides and the nucleic acids that encode them useful for preventing, diagnosing and treating e.g. cancer, inflammation and
                                                        hypertrophic cardiomyopathy, long-QT syndrome
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Sequence 1577 BP; 424 A; 410 C; 342 G; 401 T; 0 other;

Matches

617;

Conservative

0;

11.0%; 78.8%;

Score 517.4; Pred. No. 4.1 Mismatches

4; DB 23; 4.6e-136; 166;

1577; 0;

Indels Length

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Local Similarity

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RESULT 1
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  New hyaluronan-binding proteins, known as full-length WF-HABP, OE-HABP and BM-HABP, useful for treating proliferative condition
                                                                                P-PSDB; AAY93911
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Best Local Simi
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tccgtggcaccctgtttgtgccacagaacagtgggctaccgggaaataagagcctgtctg
                                                                                                                      acctgctgcaggtcctcatgtccttcccctcgctcacaaacttcctgacagaggtgctgg
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cancer related protein; HLMIT84; food additive; preservative; immunogen; antibody; bone cancer; adrenal cancer; bone marrow cancer; breast cancer; gastrointestinal cancer; liver cancer; lung cancer; urogenital cancer; immune disorder;
                                       Twenty nine nucleic acid molecules encoding human cancer associated proteins, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS00854 standard; cDNA;
                                                                                                                                                                                                          03-SEP-1999;
06-OCT-1999;
                                                                                                                                                                                                                                                     30-AUG-2000;
                                                                                                                                                                                                                                                                                   15-MAR-2001.
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DB; AAU00893.
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               Page
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                                                                                                                                                                               GENOME SCI INC
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99US-0158003.
                                                                                                                                                                                                                                                                                                                                          /product= "Cancer related
/partial
/note= "No start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                383;
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DXXXX

14-FEB-2002

(first entry)

AAS62772 standard; cDNA;

ВР

cDNA sequence

#559 encoding novel human

secreted

protein.

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RESULT 1
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      colitis, acquired immunodeficiency syndrome, AIDS), cardiovascular disorders such as myocardial ischaemias, wound healing, neurological diseases (e.g. Parkinson's disease, Albeimer's disease, cerebral anox and epilepsy) and infectious diseases such as viral, bacterial, fungal and parasitic infections. Numerous examples of each type of disorder a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mice, rabbits, goats, horses, cats, dogs, chickens or sheep. The polypeptides can also be used as a food additive or preservative
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                                                                                                       gttg-ctgtgcccacccagtacagcttcctcctctgacccttt
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0; Mismatches
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nes 181;
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Query Match 2.3%;
Best Local Similarity 60.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunodeficiency (SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis) and infectious disorders (e.g. hepatitis). The polynucleotide sequences of the invention are also useful in gene therapy. AAS52214-AAS52838 represent the CDNA sequences of the invention that encode for novel human secreted proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotides encoding secreted proteins useful asthma, HIV and Crohn's disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 358; 391pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-APR-2000; 2000US-195604P
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agttgccttttaggaacgtaaagtcctttaagcactcagaagccatacctcatctctctg
                                           gagatgccagccatcactcactgccacctgggccatcaactgtgaattctcagc---acc 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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470
                                                           4376
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20 В Qγ Ъ Qy DЬ γQ Вb δÃ В Qγ

4377 gttaatctgggattgtcgccagggctaaggagccatgttgcctggatacctggggggacct 4436

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                           gctgatctgggggttgtttctgtgggtgagagatgtgttg-ctgtgcccacccagtacag
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밁 530 cttcctcctctgacccttt 548 ccacctcctctgagcctat 4455

Search completed: June 17, 2002, 16:44:47 Job time: 9872 sec

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Result
                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB
Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title:
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length: 2000000000
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                                                                                                                                                                                                                                                           Match
                                                                                                                                                                                                                                                                   Query
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4706
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Gapop 10.0 , Gapext 1.
     GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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   5180808-1
US-08-282-141-1
US-08-288-797-1
PCT-US95-08414-1
US-07-878-960-1
US-08-264-534-5
US-08-264-534-5
US-08-346-126-5
US-08-346-126-5
US-08-832-384-1
US-08-893-828-5
PCT-US95-03747-1
US-08-225-477B-1
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US-08-242-097-1
US-09-206-695-1
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US-08-001-078A-2
US-08-463-218-2
PCT-US94-0025-3-2
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Compugen
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Sequence 1, Appli
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0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8
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Sequence 16, Appl	Sequence 16, Appl	Sequence 4, Appli	Sequence 1, Appl	Sequence 3, Appli	Sequence 7, Appli	Patent No. 5340934	Sequence 14, Appl	Patent No. 5340934	Sequence 1, Appli	Sequence 17, Appl	Sequence 17, Appl	Sequence 1, Appli					

ALIGNMENTS

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RESULT 1
US-08-024-868-1
                                                                                                                                                                                             NAME: Livnat, Shmuel
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: VILC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-628-5197
TELEPHONE: 212-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Applic Patent No. 5386013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATEN: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: Browdy and Neimark
STREET: 419 Seventh Street, NW
                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lee, Tae Ho
APPLICANT: WisniewsKi, Hans Georg
APPLICANT: Vilcek, Jan
TITLE OF INVENTION: Cytokine-Induc
TITLE OF INVENTION: Coding Therefo
                  FEATURE:
                                                                                         ORIGINAL SOURCE:
                                                                                                        TOPOLOGY: 1 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 419 Sevent
CITY: Washington
STATE: DC
COUNTRY: US
ZIP: 20004
                                                                                                                                                             LENGTH:
TYPE: n
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                                  CELL TYPE:
                                                                      ORGANISM:
                                                                                                                       TOPOLOGY: linear
NAME/KEY:
                                                                                                                                                           H: 1414 base pairs nucleic acid
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                                                                      Homo sapiens
CDS
                                  Fibroblast
FS-4
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                                                                                                                                                                                                                                                                                        COMPUTER: THE PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIAN PC-DOS/MS-DOS APPLICATION NUMBER: US/08/242,097 FILING DATE: 13-MAY-1994 CLASSIFICATION 435

ATTORNEY/AGENT TO THE PROPERTY OF THE PROPERTY ASSET OF THE PROPERTY 
                                                      ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LEE20
TELECOMMUNICATION INFORMATION:
TELECHONE: 212,628-5197
TELECHONE: 212,737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 171; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Applic
Patent No. 5846763
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lee, Tae HO
APPLICANT: Wisniewski, Hans Georg
APPLICANT: Vilcek, Jan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175
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ZIP: 20004
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CITY: Washing
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E: Browdy and Neimark
419 Seventh Street, N.W., Suite 300
ashington
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Pred. No. 2.5e-10;
0; Mismatches 167;
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 69.899
; OTHER INFORMATION:
US-08-242-097-1
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US-09-206-695-1
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Best Local Similarity
Matches 171; Conserv
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                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 13-MAY-1994
                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/206,695
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                             ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Vilcek, Jan
TITLE OF INVENTION: Cyl
TITLE OF INVENTION: The
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
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                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                               CITY: Washington
                                                                                                                  CLASSIFICATION:
                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                  20004
           BROWDY, Roger RATION NUMBER:
                                                                                                                                                                                                                                                                                                                                  419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lee,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wisniewski, Hans Georg
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50.6%;
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: 25,618
                                                                               US/08/242,097
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Pred. No. 2.5e-10;
0; Mismatches 167;
                                                                                                                                                                                                                                                                                                                                  Suite 300
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Best Local Similarity
Matches 171; Conserv
                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08001078A Patent No. 5872094
                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: Goetinck, Paul F.

APPLICANT: Tondravi, M., Mehrdad

APPLICANT: Binette, Francois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-737-3528 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3308
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: LEE26/VILCEK=1B TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                               NUMBER OF SEQUENCES:
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CELL TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM:
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TELEFAX: 212-737-3528
                                                                                        COUNTRY:
                                                                                                                         CITY: BOSTON
                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
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                                                                       02109
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                                                                                                                                             60 STATE STREET, Suite 510
                                                                                          USA
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FS-4
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                                                                                                                                                                                                                                                                                                                                                                                                                               452
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
1.ENGTH: 100 base pairs
                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Goetin
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FILING DATE: 06-JAN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L
REGISTRATION NUMBER: 35,965
               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
FILING DATE: 05-JUNE-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3232 tttgacaaagccaaagaagcctgtgccaaagaagctgcgaccatagccacctacaaccag 3293
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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APPLICANT:
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                                                                                                                              COMPUTER READABLE FORM:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII text
                                                                                                                                                                                              STREET: 60 STON
                                                                                                              MEDIUM TYPE:
                                                                                                                                                             COUNTRY:
                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
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                                                                                                                                                                                Massachusetts
                                                                                                                                                                                                              60 STATE STREET, Suite 510
                                                                                                                                                               USA
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(617) 227-5941
                                                                                                                                                                                                                                                                                            Binette, Francois
VENTION: METHODS FOR PROMOTING CARTILAGE MATRIX
                                                                                                                                                                                                                                                                                                                              Tondravi, Mehrdad
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                                                                                                           Floppy disk
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52.7%;
                                                                                                                                                                                                                                                                                 FORMATION
                               US/08/463,218
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Pred. No. 3.3e-07;
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APPLICATION NUMBER: US 0 FILING DATE: 06-JAN-1993 ATTORNEY/AGENT INFORMATION:

JMBER: US 08/001,078 06-JAN-1993

Myers, Paul L.

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PCT-US94-00253-2
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                                                                                                                                  APPLICATION NUMBER: US 08/0
FILING DATE: 06-JAN-1993
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1400 base pairs
TYPE: nucleic acid
 Best Local Similarity Matches 157; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application PC/TUS9400253 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.3%;
Best Local Similarity 52.7%;
Matches 157; Conservative
                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                        APPLICATION NUMBER: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3406
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                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII (text)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                     STRANDEDNESS:
                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gggatcgtagactacggatccagggccaacaagagtgaaatgtgggatgtcttctgtt 3463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cgggttgcctacccgactacgtatgcctctcagaagtgtggtg-----caaacgttgtt 3405
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     Conservative
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                                                                                                       linear
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                1.3%;
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Score 60; DB 5
Pred. No. 3.3e-
0; Mismatches
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Pred. No. 3.3e-07;
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 3.3e-07;
ches 135;
                                   DB 5;
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                                   Length 1400;
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                                                                                                                                                                                                                           APPLICATION NUMBER: EP 91
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,76
                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER,
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOM
                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pair
                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 30 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
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                    IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                      TOPOLOGY: li
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CLONE:
                                                                       TYPE:
                                                                                                                                                         TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
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                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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Query Match

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Score

44.2;

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Length 7218;

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RESULT 8
US-08-232-463-14
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Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                ZIP: 22313-0299

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIKG SYSTEM: PC-DOS/MS-DOS
               NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
                                                             ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SCHEIFLINGER, APPLICANT: FALKNER, F. G.
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                                                                                                FILING DATE:
APPLICATION NUMBER: EP 91
FILING DATE: 26-AUG-1991
                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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1800 Diagonal Road,
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(703)836-9300
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)2; Mismatches 215;
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                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08225477B Patent No. 5635370
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
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                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" 1.44 Mb diskette
                                                                                                                                                                                                                                                            APPLICANT: Susan Hockfield
APPLICANT: Diame M. Jaworski
TITLE OF INVENTION: BEHAB, A Brain Hya-
TITLE OF INVENTION: luronan-Binding Pro
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          APPLICATION NUMBER: US/OFFILING DATE: April 8, 19
ATTORNEY/AGENT INFORMATION:
                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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TELEX: 8
                                                                             COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                       SOFTWARE:
                                                                                                               MEDIUM TYPE:
                                                                                                                                               ZIP:
                                                                                                                                                           COUNTRY:
                                                                                                                                                                        CITY: Stamford
STATE: CT
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Mary M. Krinsky
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                                                                                                                                                           United States
                                                                      Word Processor
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Bedford Street
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                                         US/08/225,477B
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Best Local Similarity
Matches 100; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application PC/TUS9504353 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 203-327-1096
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                          APPLICATION NUMBER: 08/2:
FILING DATE: April 8, 199
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                             OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processor
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: St. Onge Steward Johnston & Reens
STREET: 986 Bedford Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3274 atagccacctacaacctacgctctcctatgcccagaaggccaagtatcacctgtgctcggcc 3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3214 ggccagtacaaactgacatttgacaaagccaaagaagcctgtgccaaagaagctgcgacc 3273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DESCRIPTION: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 203-324-6155
                                                                                                             FILING DATE: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" 1.44 Mb diskette
                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3394 gcaaacgttgttgggatc 3411
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                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Susan Hoc
APPLICANT: Diane M.
 TELECOMMUNICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE: cat cortex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               945 GGAGACATGGATGGCTTC 962
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                                                                                                                                                                                                                                                                                                              CITY: Stamford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 32
                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                 COMPUTER:
                                                                                                                                                                                                                                                                 ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                 REFERENCE/DOCKET
                                REGISTRATION NUMBER:
                                                NAME:
                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ggctggctggagagtgggggttgcctacccgactacgtatgcctctcagaagtgtggt 3393
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                                                                                                                                                                                                                                                                 06905
                                            Mary M. Krinsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
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                                                                                                                                                                                                                                                                               United States
                                                                                                                                                                                                                                                                                                                                                                                                                                              Susan Hockfield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cat brain BEHAB
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                                                                                                                                                                                                             IBM PC
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INFORMATION
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BEHAB, A Brain Hya-
luronan-Binding Protein
                                                                                                                                                PCT/US95/04353
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                                                                              08/225,477
8, 1994
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               1751-P0004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1519;
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QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                             FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: 07/922,911
APPLICATION OATE: 03 August 1992
TTING DATE: 03 August 1992
TTING TON: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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TELEFAX: 203-327-1096
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MARGOLIS, Richard APPLICANT: RAUCH, Uwe APPLICANT: MARGOLIS, Renee K.
                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                  SOFTWARE: PatentIn Rel-
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3394
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                                  ATTORNEY/AGENT INFORMATION: NAME: Browdy, Roger L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE: cat cortex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           885
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                                                                                                                                                                                                                COMPUTER: IBM PC
OPERATING SYSTEM:
               NAME: Browdy, Roger L. REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                         ZIP:
                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                          CITY:
                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                      STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gcaaacgttgttgggatc 3411
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                                                                                                                                                                                                                                                                                                                                   Washington
                                                                                                                                                                                                                                                                                         20004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08340428B
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419 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                       U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                    PatentIn Release #1.0,
                                                                                                                                                                                                                                 IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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   NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.9%;
50.5%;
                                                                                                                                                                                                                                                                                                                                                                                                     NEUROCAN AS A CHONDROITIN SULFATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Richard U.
                                                                                                                                                   5648465ember 1994
                                                                                                   07/922,911
                                                                                                                                                                     US/08/340,428B
Margolis=1A
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Pred. No. 0.092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
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TELEFAX: 202-737-3528 INFORMATION FOR SEQ ID NO:

TELEPHONE:

TELECOMMUNICATION INFORMATION:

202-628-5197

SEQUENCE CHARACTERISTICS:

LENGTH:

5191 base pairs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/922,911
FILING DATE: 03-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: CLONING, TITLE OF INVENTION: NEUROCAN NUMBER OF SEQUENCES: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3160 gacctctacttccaggaccacgaccgtaggagtattccatctacgctccccactgggccag 3219
                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MARGOLIS, Renee K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            704 CTCTCAGACCGCACGGTCCGGTACCCGATCAC 735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
                                                                 REFERENCE/DOCKET NUMBER:
                                                                               NAME: Townsend, Guy K
REGISTRATION NUMBER:
                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 03-AU
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STRANDEDNESS: sing
                            TELEPHONE:
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                                                                                                                                                                                                                                                                                                                       20004
                                                                                                                                                                                                                                                                                                                                                      D.C
                                                                                                                                                                                                                                                                                                                                                                                    419 Seventh Street, N.W
               : 202-628-5197
202-737-3528
                                                                                                                                                                                                                                                                                                                                     U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RAUCH, Uwe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MARGOLIS, Richard U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                      Browdy and Neimark
                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                 03-AUG-1993
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49.5%;
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                                                                           34,033
                                                             Margolis=1A PCT
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                                                                                                                                                                                                                                  Version #1.25
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RESULT 1:
5180808-1
RESULT 14
US-08-282-141-1
                                                                                                                                  Db
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                                                                                                                                                                                                                               QY
                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Patent No. 5180808
; APPLICANT: RUOSLAHTI, ERKKI I.
TITLE OF INVENTION: VERSICAN CORE PROTEIN, NUCLEIC ACID
;SEQUENCES ENCODING THE SAME, NUCLEIC ACID PROBES, ANTI-VERSI
;ANTIBODIES, AND METHODS OF DETECTING THE SAME
;NUMBER OF SEQUENCES: 4
;CURRENT APPLICATION DATA:
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; LOCATION:
PCT-US93-07306-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO:1
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 110; Conserv
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Best Local :
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LENGTH: 5191 base pair
                                                                                                                                                                                                                                 3250
                                                                                                                                                                                                                                                                                  3190 gtattccatctacgctccccactgggccagtacaaactgacatttgacaaagccaaagaa 3249
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FILING DATE: 27-NOV-1989
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TOPOLOGY: linear
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                                                                                 acgtatgcctctcagaagtgtggtgcaaacgttgttgggatcgtag
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                                                                                                                              gatggatttgagcagtgtgacgcaggctggctggctgatcagactgtcagatatcccatc 896
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Similarity 49.5%;
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48.78;
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Pred. No. 0.43;
0; Mismatches 116.
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Sequence 1, Application US/08282141

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Matches
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM:PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS: ADDRESS: Amgen Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 2461 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            579 GGGGGCCGGCTCTGCGACAAAGATGTCAACGAATGCAGCCAGGAGAACGGGGGGCTGCCTC 638
                                                                                                                                                                                                                                                                                                                                                                                                                                          699 TCCTCTGATGGCAGGACCTGCCAAGACATAGACGAGTGCGCAGAC 743
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CITY: Thousand Oaks
STATE: California
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TOPOLOGY: unl
                                                                                                                                  STREET: 620 Newport
CITY: Newport Beach
STATE: CA
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les 86; Conserv
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                                                                                                COUNTRY: U. ZIP: 92660
                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                       E: Knobbe, Martens, Olson and Bear 620 Newport Center Drive, Sixteenth Floor
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Manfioletti, Guidalberto
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Avanzi, Giancarlo
                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                    Anthony F. Richard
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Search completed: June 17, 2002, 16:36:14 Job time: 11744 sec
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                                                                                                                                                                                                                             Query Match 0.8%;
Best Local Similarity 62.8%;
Matches 59; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                             1922 toactgtottotggcotacggacaaagccotggaagcottgcccccagagcagcagcaggact 1981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: TI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                          1982 tcctgttcaatcaagacaacaaggacaagctgaa 2015
                                                                                                                                                          413 TCACCATCTTCGCCCCTAGCAACGAGGCCTGGGCCTCCTTGCCAGCTGAAGTGCTGGACT 472
                                                                                        473 CCCTGGTCAGCAATGTCAACATTGAGCTGCTCAA 506
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TOPOLOGY: lim
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EDNESS: single
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1264.5
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1109.5
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DB
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2710.5
2701.5
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Copyright (c) 1993 - 2000 Comp
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Novel human diagno	ABG 20414	22	3150	4.8	375.5
Human	AAB19791	21	3110	4 4 0 0 0	377.5
Human	AAY15460	20	3110		377.5
Merosin major	AAR71730	16	3110	4.8	377.5
Human	AAB19792	21	3089	4.8	377.5
Human	AAB19794	21	3088		377.5
Human	AAB66267	22	1050		378
Human	AAM50209	22	1118		395
Sequence	AAR38304	14	1404		395.5
Human	AAY59597	21	1218	5.1	399.5
Human	AAW87894	20	1218	5.1	399.5
Human	AAW44301	19	1218	5.1	399.5
Proliferation	AAW18354	18	1218	5.1	399.5
Human Serrate-1	AAW05833	17	1218	5.1	399.5
Human Jagged	AAW40827	19	1208	5.1	399.5
Proliferation	AAW18352	18	1187	5.1	399.5
Human JAGGED1	AAW87896	20	1010	5.1	399.5
Proliferation	AAW18351	18	1036		401.5
Chick Serrate	AAY59599	21	1193		410
Chick	AAW05835	17	1193	5.2	410
Drosophila	AAY59600	21	1404		413.5
Drosophila	ABB61998	22	1404		414.5
Drosophila melanog	ABB64261	22	3396		431
Mus musculus notch	AAW95557	20	1964		438.5
Partial human Notc	AAW68510	19	1872		440
Human	AAM39043	22	4618		441
Human Notch2	AAY06816	20	2471		450
Drosophila melanog	ABB70878	22	3680	٠	453.5
Human	AAB08932	21	387		455.5
Human	AAW49698	19	32		469
Drosophila melanog	ABB60266	22	2703	6.2	8
Novel	ABG06402	22	91	٠	496.5
Antigen	AAR05222	11	1.8	7.5	93.

ALIGNMENTS

RESULT AAY93910

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AAY93910 standard; Protein;

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AΑ

AAY93910;

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Key
Domain
                                                                                                                                                                                              Hyaluronan-binding protein WF-HABP; OE-HABP; BM-HABP; proliferative condition; metastasis; inflammation; ischemia; host defence dysfunction; immune surveillance dysfunction; arthritis;
                                                                                                                                                                                                                                   A human hyaluronan-binding protein, designated WF-HABP
                                                                                                                                                                                                                                                        03-OCT-2000
         Domain
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                                                                                                                                                                                       multiple sclerosis; autoimmunity; immune dysfunction; allergy
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465.478
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-14 523
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The present sequence represents a hyaluronan-binding protein. I specification describes four hyaluronan-binding protein, known WF-HABP, OE-HABP, and BM-HABP. The polypeptides are us for treating diseases such as proliferative conditions, metastate
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                                                       New hyaluronan-binding proteins, known as full-length WF-HABP, WF-HABP, OE-HABP and BM-HABP, useful for treating proliferative conditions, metastasis, inflammation, ischemia, arthritis and multiple sclerosis -
                                                                                      WPI; 2000-452376/39
N-PSDB; AAA57362.
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16-NOV-2000;
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Novel human polypeptides and the nucleic acids that encode them useful for preventing, diagnosing and treating e.g. cancer, inflammation and
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N-PSDB; AAF87119

Claim 1; Page 29-30; 141pp; English

cc and which patients may need restorative therapy. The NOVX protein may calso be used as antigens in the production of antibodies (Abs) against convex and in assays to identify modulators of NOVX expression and cativity. The anti-NOVX Abs and antagonist are used to down regulate expression and activity. The anti-NOVX Abs are used for detecting the presence of NOVX in samples. Disorders that may be prevented, diagnosed and/or treated vary depending on the NOVX protein. NOVI, expression by rectifying mutations or deletions in a patient's genome that affect the activity of protein by expressing inactive proteins or t supplement the patients own production of protein. They are used to produce NOVX proteins, by inserting the nucleic acid into a cell and culturing it to express the protein. The DNA may be used as DNA probes i assays to detect and quantitate the presence of smillar DNAs in samples. Cytostatic; contraceptive; antiinflammatory; immunomodulatory; and cardiovascular activities. The sequences may be used in the prevention diagnosis and treatment of diseases associated with inappropriate NOVX cellular adhesion disorders. NOV6-10 are homologous to EGF-like fibrillin proteins and are used to treat cardiovascular disease e.g hypertrophic cardiomyopathy, long-QT syndrome and marfan syndrome. used to treat cancers, inflammatory disorders, immune disorders and the s sequence is the NOV8 protein. The invention relates to MOV1-NOV16 proteins, and their coding sequences. The proteins have They may be used to treat disorders associated with decreased in the prevention, ç

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78.8%;
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Pred. No. 1.5
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e-175;
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This sequence is the NOV6 protein. The invention relates to the NOV1-NOV16 proteins, and their coding sequences. The proteins have Cytostatic; contraceptive; antiinflammatory; immunomodulatory; and cardiovascular activities. The sequences may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate NOVX expression. They may be used to treat disorders associated with decrease expression by rectifying mutations or deletions in a patient's genome that affect the activity of protein by expressing inactive proteins or supplement the patients own production of protein. They are used to produce NOVX proteins, by inserting the nucleic acid into a cell and culturing it to express the protein. The DNA may be used as DNA probes assays to detect and quantitate the presence of similar DNAs in samples and which patients may need restorative therapy. The NOVX protein may
                                                                                                                                                                                                                                                                                                                                                                                                                                    19-NOV-1999;
29-NOV-1999;
08-MAR-2000;
16-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOV: Cytostatic; contraceptive; antiinflammatory; immunomodulatory; cardiovascular; casein kinase II phosphorylation site; contraception; serine/threonine kinase; Peutz-Jephers syndrome; cellular poliferation; epidermal growth factor; cell development; apoptosis; cell adhesion; growth migration; cell structure; motility; cancer; immune disorder; inflammatory disorder; cellular adhesion disorder; long-OT syndrome; cardiovascular disease; hypertrophic cardiomyopathy; marfan syndrome; therapy; NOV1; NOV2; NOV4; NOV5; NOV6; NOV7; NOV8; NOV9; NOV10; NOV11; NOV12; NOV13; NOV14; NOV15; NOV16.
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                                                                                                                                                                                                                                                                           Novel human polypeptides and the nucleic acids that encode them useful for preventing, diagnosing and treating e.g. cancer, inflammation and
                                                                                                                                                                                                                                                                                                                                                                                                        (CURA-) CURAGEN
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RESULT
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CC NOV7, NOV9-11 and NOV13-16 have casein kinases II phosphorylation sites CC characteristic of serine/threonine kinases, and are used to treat CC kinase-related disorders (e.g. Peutz-Jeghers syndrome, cellular CC kinase-related disorders (e.g. Peutz-Jeghers syndrome, cellular CC proliferation and contraception). NOV2-3, NOV6 and NOV8 are homologous to CC the epidermal growth factor (EGF)-like super family and are involved in, cell regulation of cell development, apoptosis, cell adhesion, growth CC migration, cell structure and motility and protein management, and are used to treat cancers, inflammatory disorders, immune disorders and CC cellular adhesion disorders. NOV6-10 are homologous to EGF-like CC cellular adhesion and are used to treat cardiovascular disease e.g.
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NNTCVCNLNYEGDGITCTVVDFCKQNNGGCAKVAKCSQKGTQVSCSCKKGYKGDGYSCIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLPRSASWKTLQGSELSVRCGTGSDIGELFLNEQMCRFIHRGLLFDVGVAYGIDCLLMNP
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                                        DASCADLYFQDTTVGVFHLRSPLGQYKLTFDKAKEACAKEAATIATYNQLSYAQKAKY
                                                                                                                                                                                                                                                                 RFGPDCQPRSCSEHGQCDEGITGSGECLCETGWTAASCDTPTAVFAVCTPACSVHATCTE
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                                                                                idpcadglnggchehatckmtgpgkhkceckshyvgdglncepeqlpidrclqdngqcha
                                                                                                                          IDPCADGVNGGCHEHATCRMTGPGKHKCECKSHYVGDGVDCEPEQLPLDRCLQDNGQCHP 1048
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78.6%;
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A human hyaluronan-binding

protein,

designated

BM-HABP

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Matches
                                                                                                                         Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                               OE-HABP and BM-HABP, useful for treating proliferative conditions, metastasis, inflammation, ischemia, arthritis and multiple sclerosis
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                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                             inflammation, ischemia, host defence dysfunction, immune surveillance dysfunction, arthritis, multiple sclerosis, autoimmunity, immune
                                                                                                                                                                                                                                                         The present sequence represents a hyaluronan binding protein. The specification describes four hyaluronan binding protein, known as Specification describes, and BM-HABP. The polypeptides are useful for treating diseases such as proliferative conditions, metastasis,
                                                                                                                                                                                                                                                                                                                                                                             New hyaluronan-binding proteins, known as full-length WF-HABP, WF-HABP, OE-HABP and BM-HABP, useful for treating proliferative conditions,
                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hastings GA,
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                 RSPLGQYKLTFDKAKEACAKEAATIATYNQLSYAQKAKYHLCSAGWLESGRVAYPTTYAS
                                                                          MTGPGKHKCECKSHYVGDGVDCEPEQLPLDRCLQDNGQCHPDASCADLYFQDTTVGVFHL 1067
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                                              mtgpgkhkceckshyvgdglncepeqlpidrclqdngqchadakcvdlhfqdttvgvfhl
   280;
                                                                                                                        Similarity
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                                                                                                          Conservative
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CAN NAT RED
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29-NOV-1999;
08-MAR-2000;
16-NOV-2000;
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                                     This sequence is the NOV2 protein. The invention relates to the NOV1-NOV16 proteins, and their coding sequences. The proteins have Cytostatic; contraceptive; antiinflammatory; immunomodulatory; and cardiovascular activities. The sequences may be used in the prevention diagnosis and treatment of diseases associated with inappropriate NOVX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               produce NOVX proteins, by inserting the nucleic acid into a cell and culturing it to express the protein. The DNA may be used as DNA probes i assays to detect and quantitate the presence of similar DNAs in samples, and which patients may need restorative therapy. The NOVX protein may be used as antigens in the production of antibodies (Abs) against any protein and the production of antibodies (Abs) against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOVX and in assays to identify modulators of NOVX expression and activity. The anti-NOVX Abs and antagonist are used to down regu
                                     growth migration; cell structure; motility; cancer; immune disorder; inflammatory disorder; cellular adhesion disorder; long-QT syndrome;
                                                                                                                    NOV; Cytostatic; contraceptive; antiinflammatory; immunomodulatory; cardiovascular; casein kinase II phosphorylation site; contraception;
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                      cardiovascular
                                                                          epidermal growth factor; cell development; apoptosis; cell adhesion;
                                                                                               serine/threonine kinase; Peutz-Jeghers syndrome; cellular proliferation;
                                                                                                                                                                                                                                                                                                       AAB83365 standard;
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78.3%;
                  hypertrophic cardiomyopathy;
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4; Mismatches
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  NOV6;
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Вþ ρy B QΥ

569 VLSSDIISTNGVIHVIDKLLSPKNLLITPKDALGRVLQNLTTVAANHGYTKFSKLIQDSG

RIKDWDQQGLMSQVLRYHVVGCQQLLLDNLKVTTSATTLQGEPVSISVSQDTVFINNEAK 568 qvkdwdkyglmpqvlryhvvachqlllenlklisnatslqgepivisvsqstvyinnkak

Matches

Conservative

37;

Mismatches

Score 1318.5; D Pred. No. 4e-81;

DΒ 39; 22;

Length

<u>,</u>

Gaps

1;

127

628

8

Best Local Similarity

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Cytostatic; contraceptive; antiinflammatory; immunomodilatory; and criefly sequences may be used in the prevention, CC diagnosis and treatment of diseases associated with inappropriate NOVX CC expression. They may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of protein by expressing inactive proteins or to CC supplement the patients own production of protein frequency cell and CC culturing it to express the protein of protein associated with decreased CC unituring it to express the protein of protein frequency cell and CC culturing it to express the protein. The DNA may be used as DNA protein may cell assays to detect and quantitate the presence of similar DNAs in samples, CC and which patients may need restorative therapy. The NOVX protein may CC also be used as antigens in the production of antibodies (Abs) against CC NOVX and in assays to identify modulators of NOVX protein may CC activity. The anti-NOVX Abs and antagonist are used to down regulate presence of NOVX in samples. Disorders that may be prevented, diagnosed and/or treated vary depending on the NOVX protein. NOV1, NOV3, NOV5, NOV7, NOV9-11 and NOV13-16 have casein kinase II phosphorylation sites CC characteristic of serine/threonine kinases, and are used to treat CC winase-related disorders (e.g. Peutz-Jeghers syndrome, cellular country cell development, apoptosis, cell adhesion, growth factor (EGF) like super family and are involved in, cell structure and motility and protein management, and are used to treat the country inflammatory disorders, immune disorders and country in the modulatory of cell adhesion, growth to read to treat cancers, inflammatory disorders, immune disorders and country in the modulation of cell development, apoptosis, cell adhesion, growth country in the modulation of cell development and country to EGF-like
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08-MAR-2000;
16-NOV-2000;
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N-PSDB; AAF87120.
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Sequence
                                         hypertrophic cardiomyopathy, long-QT
                                                                                         cellular adhesion disorders. NOV6-10 are homologous to EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 32-33; 141pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAY-2001
                                                                fibrillin proteins and are used to treat cardiovascular disease
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2000US-0715417
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Cytostatic; contraceptive; antiinflammatory; immunomodulatory; and cardiovascular activities. The sequences may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate NOVX expression. They may be used to treat disorders associated with decreas expression by rectifying mutations or deletions in a patient's genome that affect the activity of protein by expressing inactive proteins or supplement the patients own production of protein. They are used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      growth migration; cell structure; motility; cancer; immune disorder; inflammatory disorder; cellular adhesion disorder; long-QT syndrome; cardiovascular disease; hypertrophic cardiomyopathy; marfan syndrome; therapy; NOV1; NOV3; NOV3; NOV4; NOV5; NOV6; NOV7; NOV8; NOV9; NOV10; NOV11; NOV12; NOV14; NOV15· NOV16
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                                                                                                  This sequence is the NOV7 protein. The invention relates to the NOV1-NOV16 proteins, and their coding sequences. The proteins
                                                                                                                                                  Claim
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16-NOV-2000;
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DB; AAF87118.
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                                                                                                                                                                                        human polypeptides and the nucleic acids that encode them useful reventing, diagnosing and treating e.g. cancer, inflammation and
                                                                                                                                                Page
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Best Local
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therapy; nov12;
                  inflammatory disorder; cellular adhesion disorder; lnmune disorder; cardiovascular disease; hypertrophic cardiomyopathy; marfan syndrome; therapy; NOV1; NOV2; NOV3; NOV4; NOV5; NOV6; NOV6; NOV7: NOV8. NOV8.
                                                                                     NOV; Cytostatic; contraceptive; antiinflammatory; immunomodulatory; cardiovascular; casein kinase II phosphorylation site; contraception; serine/threonine kinase; Peutz-Jeghers syndrome; cellular proliferation; epidermal growth factor; cell development; apoptosis; cell adhesion; growth migration; cell structure; motility; cancer; immune disorder; growth migration; cell structure; motility; cancer; immune disorder;
                                                                                                                                                                                                                  NOV3
                                                                                                                                                                                                                                                                                             AAB83359;
                                                                                                                                                                                                                                                                                                                                   AAB83359 standard; Protein; 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234;
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73.1%;
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Pred. No. 1.1
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Qy
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                                                                                                                                                                                                                                                                                                              Cytostatic; contraceptive; antinfiammatory; immunomodulatory; and cried of diseases associated with inappropriate NOVX contraceptive; antinfiammatory; immunomodulatory; and diseases associated with inappropriate NOVX contraceptive; and treatment of diseases associated with inappropriate NOVX contraceptive; and diseases associated with inappropriate NOVX contraception. They may be used to treat disorders associated with decreased contraception. They may be used to treat disorders associated with decreased contraception by rectifying mutations or deletions in a patient's genome contraception. They are used to produce NOVX proteins, by inserting the nucleic acid into a cell and contraception; by inserting the nucleic acid into a cell and contraception in the production of antibodies (Abs) against condition by expressing inactive probes in assays to detect and quantitate the presence of similar DNAs in samples, and which patients may need restorative therapy. The NOVX protein may cartivity. The anti-NOVX Abs and antagonist are used to down regulate conversation and activity. The anti-NOVX abs are used for detecting the conversation and activity. The anti-NOVX abs are used for detecting the conversation and activity. The anti-NOVX protein. NOV1, NOV1, NOV2, NOV2-11 and NOV1-16 have casein kinase II phosphorylation sites characteristic of serine/threonine kinases, and are used to treat conversation and contraception. NOV2-3, NOV5 and NOV8 are homologous to the epidermal growth factor (EGF)-like super family and are involved in, e.g. regulation of cell development, apoptosis, cell adhesion, growth migration, cell structure and motility and protein management, and are used to treat cancers, inflammatory discorders, immune disorders and cellular candidates and are used to treat cancers, inflammatory discorders and are homologous to EGF-like therefore the cardiovocathy. Inco-07 syndrome and marfan syndrome.
                                                                                                                                                              Matches
                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAR-2000;
16-NOV-2000;
                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence is the NOV3 protein. The invention relates the NOV1-NOV16 proteins, and their coding sequences. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human polypeptides and the nucleic acids that encode them useful for preventing, diagnosing and treating e.g. cancer, inflammation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200136638-A2
                                                                                                                                                                                                                                                                                                      hypertrophic cardiomyopathy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CURA-) CURAGEN CORP.
                                       924
                                                                                                  864 LCWHGREGPDCQPRSCSEHGQCDEGITGSGECLCETGWTAASCDTPTAVFAVCTPACSVH 923
    61
                                                                                                                                                                                   Local Similarity
                                                                               _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-648134/74
DB; AAF87114.
atckenntcecnldyegdgitctvvdfckqdnggcakvarcsqkgtkvscscqkgykgdg
                  ATCTENNTCVCNLNYEGDGITCTVVDFCKQNNGGCAKVAKCSQKGTQVSCSCKKGYKGDG
                                                                               mcwpgrfgpdclpcgcsdhgqcddgitgsgqclcetgwtgpscdtqavlsavctppcsah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Page 14-17; 141pp; English
                                                                                                                                                                202;
                                                                                                                                                                                                                                                                244 AA;
                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000WO-US31543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-187844P
2000US-0715417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lichenstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-166336P
99US-167785P
                                                                                                                                                                                 15.4%;
84.2%;
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                                                                                                                                                              19;
                                                                                                                                                                                 Score 1209; DB 22
Pred. No. 3.7e-74;
                                                                                                                                                                                                                                                                                                      long-QT syndrome and marfan syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vernet C,
                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fernandes
                                                                                                                                                                                                      DB 22;
                                                                                                                                                                19;
                                                                                                                                                                                                      Length
                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to
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                                                                                                                                                              0;
                                                                                                                                                              Gaps
                                         983
                                                                               60
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RESULT
AAB42164
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02-APR-1999;
05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antiihyroid; antirhammatic; ene therapy; cancer; proliferative disorder; hypottension neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; astima; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB42164 standard;
the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers,
                                                                       antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining
                                                                                                                                                                                      AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-602362/57.
N-PSDB; AAC76373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vulnerary; antipsoriatic; antiparkinsonian;
anticonvulsant; osteopathic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human ORFX ORF1928 polypeptide sequence SEQ ID NO:3856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-FEB-2001
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                                                                                                                                                                                                                                                                 Claim 11;
                                                                                                                                                                                                                                                                                                  useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-2000; 2000WO-US08621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200058473-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bone damage; cartilage damage; antiinflammatory disease; thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; open
                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids and peptides derived from open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mmunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hscteidpcadglnggchehatckmtgpgkhkceckshyvgdglncepeqlpidrclqdn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YSCIEIDPCADGVNGGCHEHATCRMTGPGKHKCECKSHYVGDGVDCEPEQLPLDRCLQDN 1043
                                                                                                                                                                                                                                                                Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reading frame; ORFX; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0540763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first
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99US-0127728
                                                                                                                                                                                                                                                                3007-3008; 5507pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nootropic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypertension;
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RESULT :
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Best Local Similarity
Matches 217; Conser
19-NOV-1999;
29-NOV-1999;
08-MAR-2000;
16-NOV-2000;
                                                                                                                                                                                              therapy; he nov12;
                                                                                                                                                                                                                                                                               NOV; Cytostatic; contraceptive; antiinflammatory; immunomodulatory; cardiovascular; casein kinase II phosphorylation site; contraception; serine/threonine kinase; Peutz-Jeghers syndrome; cellular proliferation; epidermal growth factor; cell development; apoptosis; cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   allergies, aplastic anaemia, burns, wounds, bone and cartilage damage nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, choolesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma,
                                                                                                                                                                                                         cardiovascular disease;
therapy; NOV1; NOV2; NOV
NOV11; NOV12; NOV13; NOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1149
                                                                                                                                                                                                                                                     growth migration; cell structure; motility; cancer; immune disorder; inflammatory disorder; cellular adhesion disorder; long-QT syndrome;
                                                                                                                                                                                                                                                                                                                                                                 NOV10 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB83366 standard; Protein;
                                                                                17-NOV-2000;
                                                                                                                                             WO200136638-A2
                                                                                                                                                                             Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GIFCAVVLVTGAIALAAYSYFRLKQRTTGFQRFDQKRTLMSWLLAS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLKHLTDLSIRGTLFVPQNSGLPGNKSLSGRDIEHHLTNVNVSFYNDLVNGTFLRTMLGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MWDVFCYRMKDVNCTCKAGYVGDGFSCSGNLLQVLMSFPSLTNFLTEVLAFSKSSARGQA 1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a a \verb|tmatynqls| yaqkakyhlcs agwletgrvayptafasqncgsgvvgivdygprpnkse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            giffaiilvtgavalaaysyfrinrrtigfqhfeseedinvaalgkqqpenisnplyest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QLLITFSQDQLHQ--ETRFVDGRSILQWDIIAANGILHIISEPLRAPPTAATAAHSGLGT 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fleh \verb|ltdlsirgtlfvpqnsg|| igenetlsgrdiehhlanvsmffyndlvngtxpaneggk
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               99US-166336P.
99US-167785P.
2000US-187844P.
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                                                                              2000WO-US31543
2000us
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68.0%;
                                                                                                                                                                                                        se; hypertrophic cardiomyopathy; marfan syr NOV3; NOV4; NOV5; NOV6; NOV7; NOV8; NOV9; NOV14; NOV15; NOV16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1109.5;
Pred. No. 3.2e
28; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSPRISQT 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
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VLSSDIISTNGVIHVIDKLLSPKNLLITPKDALGRVLQNLTTVAANHGYTKFSKLIQDSG

187

RIKDWDQQGLMSQVLRYHVVGCQQLLLDNLKVTTSATTLQGEPVSISVSQDTVFINNEAK 568

Query Match Best Local S Matches 197

al Similarity 197; Conserv

Conservative

29;

Mismatches

Indels Length 334;

0;

Gaps

0

to

13.6%; 77.9%;

Score 1067; Pred. No. 2

.5e-64;

DB 22; 27;

509 8

Sequence

20 Вþ Qy DЬ

TLGGRCDTFTTFD

307

ll s vit d piht p v tlf wpt d qalhalpa eqqdflf nqdnkdklkeylkfhvirdakvlav between the property of the propertLLSVITDSIHTPVTVFWPTDKALEALPPEQQDFLFNQDNKDKLKSYLKFHVIRDSKALAS iis s diis tngiv hiid kllspknllitpkdnsgrilqnlttlatnngyikfsnliqdsg

247

308 749 248 689 188 629 128 569

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CC produce Novx proteins, by inserting the nucleic acid into a cell and CC culturing it to express the protein The DNA may be used as DNA probes in CC assays to detect and quantitate the presence of similar DNAs in samples, CC and which patients may need restorative therapy. The NOVX protein may CC also be used as antigens in the production of antibodies (Abs) against CC NOVX and in assays to identify modulators of NOVX expression and CC activity. The anti-NOVX Abs and antagonist are used to down regulate CC expression and activity. The anti-NOVX Abs are used for detecting the CC presence of NOVX in samples. Disorders that may be prevented, diagnosed CC and/or treated vary depending on the NOVX protein. NOV1, NOV3, NOV5, CC NOV7, NOV9-11 and NOV13-16 have casein kinase II phosphorylation sites CC characteristic of serine/threonine kinases, and are used to treat kinase-related disorders (e.g. Peutz-Jeghers syndrome, cellular CC the epidermal growth factor (BCF)-like super family and are involved in, CC e.g. regulation of cell development, apoptosis, cell adhesion, growth are used to treat cancers, inflammatory disorders, immune disorders and are used to treat cancers, inflammatory disorders, immune disorders and
                                         cellular adhesion disorders. NOV6-10 are homologous to EGF-like fibrillin proteins and are used to treat cardiovascular disease hypertrophic cardiomyopathy, long-QT syndrome and marfan syndrom \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression. They may be used to treat disorders associated with decree expression by rectifying mutations or deletions in a patient's genome that affect the activity of protein by expressing inactive proteins or supplement the patients own production of protein. They are used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis and treatment of diseases associated with inappropriate NOVX expression. They may be used to treat disorders associated with decreased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytostatic; contraceptive; antiinflammatory; immunomodulatory; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 35; 141pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human polypeptides and for preventing, diagnosing ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cardiovascular activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence is the NOV10 protein. The invention relates to the NOV1-NOV16 proteins, and their coding sequences. The proteins have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-648134/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lichenstein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequences may be used in the prevention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nd the nucleic and treating (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vernet C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e.g. cancer, inflammation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fernandes
                                              marfan syndrome
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RESULT 11
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                                                                                                                                                                              The present sequence represents a hyaluronan-binding protein. The specification describes four hyaluronan-binding protein, known as WF-HABP, WF-HABP, OE-HABP, and BM-HABP. The polypeptides are useful for treating diseases such as proliferative conditions, metastasis, inflammation, ischemia, host defence dysfunction, immune surveillance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A human hyaluronan-binding protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY93911 standard;
                                                                                                                                                                                                                                                      Claim 11; Fig
                                                                                                                                                                                                                                                                             OE-HABP and BM-HABP, usefumetastasis, inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hyaluronan-binding protein WF-HABP; OE-HABP; BM-HABP;
 1030
                                                                                                                                                                                                                                                                             New hyaluronan-binding proteins, known as full-length WF-HABP, WF-OE-HABP and BM-HABP, useful for treating proliferative conditions, metastasis, inflammation, ischemia, arthritis and multiple scleros
                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                 Hastings
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                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME
(AMNA-) AMERICAN NAT
                                                                                                                                                       dysfunction and allergy
                                              971
                                                                                                                                                                    dysfunction, arthritis,
                                                                                                                                                                             Inflammation, ischemia,
                                                                     Local Similarity 40.1 nes 162; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    defence dysfunction; immune surveillance dysfunction;
iple sclerosis; autoimmunity; immune dysfunction; alle
EPEQLPLDRCLQDNGQCHPDASCADLYFQDTTVGVFHLRSPLGQYKLTFDKAKEACAKEA 1089
                                    VSCSCKKGYKGDGYSCIEIDPCADGVNGGCHEHATCRMTGPGKHKCECKSHYVGDGVDC- 1029
                                                                                                                                                                                                                                                                                                                             2000-452376/39.
)B; AAA57363.
                     vtctclpdyegdgwscrarnpctdghrggcsehanclstglntrrcechagyvgdglqcl
                                                                                                                                                                                                                                                                                                                                                                 GA,
                                                                                                                                 457 AA;
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                                                                                                                                                                                                                                                     2A-B; 457pp; English.
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194..208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "link domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "unspecified
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                                                                                                                                                                                                                                                                                                                                                                   Tsifrina
                                                                                                                                                                   multiple sclerosis,
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                                                                                 Score 774; DB 2
Pred. No. 3e-44;
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                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                             DB 21;
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                                                                                                                                                                    autoimmunity,
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                                                                                           Length 457;
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RESULT 1
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B
                                       It is encoded by an open reading frame contained within the sequence of clone 533 which was derived from an E. tenella genomic library screened with radioactively labelled cDNA encoding the GX5401 antigen. It is of about 250 Kd. It carries several repeated peptide sequences and is rich in cysteine residues. The open reading frame also encodes a potential signal sequence for protein secretion. Also new are an expression vector contg. cloned gene, and host cells transformed with the vector. The transformed cells are used in a vaccine to immunise birds against avian coccidiosis. By labelling the peptides, they can be used as a type-specific probe. May also be used in an assay to detect a bagainst the coccidia. The Abs are used to identify transformed cells
                                                                                                                                                                                                                                                  Cloned gene or fragment encoding antigenic protein which binds with antibodies against avian coccidia. transformed cells used in vaccine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antigen GX5401FL
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                                                                                                                                                                                                                                                                                                                                                           Anderson DM,
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                                                                                                                                                                                                                        Claim 10;
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                                                                                                                                                                                                                        Page 93; Fig 14; 134pp; English
                              DNA
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shtctcnegyqgdgkkcektvgp---c--dnspcgnnamc----eatadsynctckag
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                              KHKCECKSHYVGDGVDCEPEQLPLDRCLQDNGQCHPDASCADLYFQDTTVGVFHLRSPLG
                                                            agtatcgersfcvdtqgsykceckngyrqsgedcvdvdeceadvh-tcsehatctnt-eg
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Pred. No. 4.5e-31;
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                                                                  polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (CR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics forensics can manning identification of mutations.
diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human
                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                              The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                   Claim 20; SEQ ID No 36761; 103pp; English
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food supplement; medical imaging; diagnostic; genetic (
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RSCSEHGQCDEGITGSGECLCETGWTAA - -
                                                                                                         KSKPKGVKKKCI-YNPLPFRRNVEGCQN-LCTVVIQTPRC-CH-GY-FMPDCQACP----
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                                                       GGPDTPCNNRGMCRDLYTPMGQCLCHTGF----NGTAC---ELCWHGRFGPDCQP
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Pred. No. 2.5e-24;
                             -ecscsegyalmpdgrscadidec-
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical
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capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).

[ABB57737-ABB72072]

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from

The invention relates to an isolated nucleic acid detection reagent

invention

and is

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131 EIQKNRCDNNDT------IIVRGECGK-CSQQAPCPLETKPLRETRKCIYSIYFMG 179

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RESULT 1
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Matches 272
                                                                                                                         This sequence represents the human Notch3 protein, a transmembrane receptor protein involved in lateral inhibition and regulating developmental cascades of neurogenic genes. Mutated Notch3 proteins are thought to be involved in neurological disorders, especially of the cerebral autosomal dominant arteriopathy with subcortical infarcts and leukoencephalopathy (CADASIL) type. Blocking expression of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW49698 standard;
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                                                                                                and leukoencephalopathy (CADASIL) type. Blocking expression of a mutated Notch3 gene or by substitution therapy with non-mutated Notch3 gene or protein can be used to treat CADASIL or related disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; Notch3; transmembrane receptor; lateral inhibition; requesevelopmental cascade; neurogenic gene; mutant; neurological dicerebral autosomal dominant arteriopathy; subcortical infarct;
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ylcscppgt	qhggscidl HLCSAG-WL	1131 1106
TTVGVFHLRSPLGQYKLTFDKAKEACAKEAATIAT	PDAS	04
CHEHATCRWTGPGKHKCECKSHYVGDGVDCEPEQLPLDRCLQDNGQ 	Gshceqevdpcl	999 1079
	QVSCSCKKGYKG :: yclcppgwsgrlo	970 1021
TCVCNLNYEGD	VCTPA-CSVHATCTENN	915 976
ELCWHGRFGPDCQPRSCSEHGQCDEGITGSGECLCETGWTAASCDTPTAVFA	ELCWHGRFGPDO : ! eqdlpdo	863 922
QC 	GMCRD : gscqdgvgsfscs	839 862
QNLCTVVIOTPRC-CH-GYFMP : gpapcgphgictnlagsfsctchggytgp	YNPLPFRRNVEGC ::: : qqdvdecagpa	790
quq	VAYGIDCLIMNPTL : -vqgrqcellspct	737 764
HVIRDSKALASDLPRSASWKTLQGSELSVRCGTGSDIGELFLNEQMCRF	FHVIRDSKALAS	677 734
GLLSVITDSIHTPVTVFWPTDKALEALPPEQQDFLFNQDNKDKLKSYLK : : : : : : : : : : : : : : :	KFSKLIQDSGLLSVITDS : 1:icydapggfrcvcepg	619 708
NNEAKVLSSDIISTNGVIHVIDKLLSPKNLLITPKDALGRVLQNLTTVAANHG	INNEAKVLSSDI	563 670
GLMSQ-VLRYHVVGCQQLLLDNLKYTTSATTLQGEPVSISVSQDTVF :	KDWDQQGLMSQ-VLRYHVVG : : ddcasnpctfgvcrdginrydcv-	511 622
TGDGIVCRGŚIYGELPKNPSTSQYFFQLQEHAVRELAGPGPFTVFAPL-SSSFNHEPR 	YTGDGIVCRGSIY	452 574
QTGPNQAVCNCLPKYTGDGKVCSLINVCLTNNGGCSPFAFCNYTEQDQRItlcdrnvddcspdp-chhgrcvdgias	QTGPNQAVCNCLPKYTG : : dq-pdgyecrcaegfeg	396
-NGGCSTKADCKRTTPGNRVCVCKAGYTGDGIVC-LEINPCLENHGGCDRNAECT 	ETSNGGCSTF	340 474
DVGWRGVKCDMEITTDNC-NGTCHTSANCLLDPDGKASCKCAAGFRGNGTVCTA-INAC - -	CDVGWRGVKCDMEI : : : :: cgrgytgprcetdv	282
GVNGTGTCQCGLGFNGTACETCTEGKYGIHCDQACSCVH-GRCSQGP 	GVNGTGTCQCGI	370
KRSVFIGCQPQCVRTIITRACWLASLAHNAKPAPGEVKMCALGTASV	KRSVFIGCQPQC	180 I

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Search completed: June 17, 2002, 12:30:21 Job time: 252 sec

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InterPro; IPR000152; Asx_hydroxyl.
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InterPro; IPR001881; EGF-Ca.
InterPro; IPR001438; EGF-II.
InterPro; IPR001438; EGF-II.
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{\tt GSGICVNTPGSFECECFEGYESGFMMKNCMDIDECERNPLLCRGGTCVNTEGSF---}
                     HRGLLFDVGVAYGIDC------LLM-----
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                                                              HVIRDSKALASDLPRSASWKTLQGSELSVRCGTG---
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23.5%;
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SEQUENCE
                                          MEDLINE=91304568; PubMed=185207; Maslen C.L., Corson G.M., Maddox: "Partial sequence of a candidate (Nature 352:334-337(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LHUMAN
SEQUENCE OF 813-1313 FROM MEDLINE=91304567; PubMed=1
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                                                                                                                                                                                                                                               Corson G.M., Chalberg S.C., Dietz H.C "Fibrillin binds calcium and is coded
                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-932 FROM N.A. TISSUE=Placenta, and Fibroblast; MEDLINE=94010947; PubMed=7691719;
                                                                                                                                                                                                                                                                                                                                                                                             defective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria;
NCBI_TaxID=9606;
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Pangilinan T., Bonadio J
"Genomic organization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=93372860; PubMed=8364578;
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    PubMed=1852206;
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Dietz H.C., Cu++*
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Cell 85:
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                              Dietz
"Clust
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"Fibrillin-1 mutations in
"Fibrillin-2 mutations in
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J. M
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the fibrillin gene.";
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pair from human fibrillin-1.";
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        patients
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S SER-1249; ARG-1663; SER-2221 AND SER-250834; PubMed=1301946;
Saraiva J.M., Pyeritz R.E., Cutting G.F
of fibrillin (FBNI) missense mutations
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Hollister D.W.;
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the analysis
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Stahl-Hallengren C., Ukkonen T., Kainulaine Saxne T., Tornqvist K., Peltonen L.; "An extra cysteine in one of the non-calcinfactor-like motifs of the FBN1 polypeptide variant of Marfan syndrome.";
                                                                                                                                                                                               MEDLINE=94272487; PubMed=8004112; Hayward C., Rae A.L., Porteous M.E. "Two novel mutations and a neutral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93278402; PubMed=8504310;
Hewett D.R., Lynch J.R., Smith R., Sykes B.C.;
"A novel fibrillin mutation in the Marfan syndrome which
disrupt calcium binding of the epidermal growth factor-li
Hum. Mol. Genet. 2:475-477(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
J. C
                  syndrome
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MEDLINE=94314977; Pu
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"Mutation screening of complete fibrillin-1
of five new mutations, including two in 8-cy
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94108431;
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MEDLINE=92235290; Pu
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                           Lynch J.R., se mutation
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970; PubMed=7977366;
Raghunath M., Loenng
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         31:338-339(1994)
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94:709-713(1994).
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                           PubMed=8071963;
h J.R., Child A., Sykes
utation of fibrillin in
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PubMed=8406497;
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EGF-like do
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K-2447 AND R-2511.
MEDLINE-94184368; PubMed=8136837;
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"A novel mutation in the fibrillin gene (FBN1)
arachnodactyly.";
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KCRCDSGFALDSEERNCTDIDECRISPDLC---GRGQCVNTPGDFECKCDEGYESGFMMM 1108
                                                                                                                                    DALGRVLQNLTTVAANHGYTKFSKLIQDSGLLSVI----TDSIHTPVTVFWPTDKA----
                                                                                                                                                                                                                                                 RIKDWDQQGLMSQVLRYHVVGCQQLLLD-NLKVTTSATTLQ-------
                                                                                                                                                                                                                                                                                                   DYTGD--GIVCRGSIYGELPKNPSTSQYFFQLQEHAVRELAGPGPFTVFAPLSSSFNHEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GECINNQGSYTCQCRAGYQSTL--TRTECRDIDECLQNGRICNNGRCIN---TDGSFHCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WDGVNGTG--TCQCGLGFNGTACETCTEGKYGIHCDQ-ACSCVHGRCSQGPLGDGS--CD
                             SVRCGTG----
                                                                                                            DATGRICLDIRL----
                                                                                                                                                               QVDPICGKGYSRIKGTQCEDIDECEVFPGVCKNGLCVNTRGSF----
                                                                                                                                                                                                                                                                            ESTLDPTKTICIETIKGT
                                                                                                                                                                                                                                                                                                                              PGSFVCTC-PKGFIYKPDLKTCEDIDECESSPCINGVCKNSPGSF
                                                                                                                                                                                                                                                                                                                                                  PNQAVCNCLPK---YTGDGKVCSLINVCLTN---NGGC--SPFAFCNYTEQDQRICTCKP
                                                                                                                                                                                                                                                                                                                                                                                    CALDPDICPNGICENLRGTYKCICNSGYEVDSTGKNCVDINECVLNSLLCD-NGQCRNT-
                                                                                                                                                                                                                                                                                                                                                                                                                                         RGQCIKPLFGAVTKSECCCASTEYAFGEPCQPCPAQNSAEYQALCSSGPGMTSAGSDINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \tt DGRYCKDINECETPGICMNGRCVNTDGSYRCECFPGLAVGLDGRVCVDTHMRSTCYGGYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NGTVCTAINACET - - - SNGGC - - :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNAGFHVTRDGKNCE---DMDECSIRNMCLNGMC----INEDGSFKCICKPGFQLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDVGWR-----GVKCDMEITTDNC-----NGTCHTSANCLLDPDGKASCKCAAGFR--G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRVLPVNVTDYCQLVRYLCQNGRCIPTPGSYRCECNKGFQLDLRGECIDVDECEKNPCAG
                                                                                                                                                                                         SQDTVFINNEAKVLSS---DI-------ISTNGVIHVIDKLLSPKNLLITPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                               -LEALPPEQQDFLFNQDNKDKLKSYLKFHVIRDSKALASDLPRSASWKTLQGSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probes 8:325-327(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=7870075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.3%;
21.7%;
                           SDIGELFLNEQMCRFIHRGLLF------DVGVAYG----
                                                                                                          -ETCFLRYEDEECTLPIAGRHRMDACCCSVGAAWGTEECEECP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121;
                                                                                                                                                                                                                     -CWQTVIDGRCEININGATLKSQCCSSLGAAWGSPCTL-C
                                                                                                                                                                                                                                                                                                                                                                                                             -CVCKAGYTGD--GIVCLEINPCLENHGGCDRNAECTQTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 497.5; DB 1;
Pred. No. 8e-27;
                                                      TNGKPFFKDINECKMIPSLCTHGKCRNTI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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ble for dor
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                                                                                                                                                                                                                                               -GEPVSISV
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                                                      -GSF
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FBN2_HUMAN
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                                                                                                                                 "Linkage of Marfan syndrome and a phenotypically two different fibrillin genes.";
Nature 352:330-334(1991).
                                                                                                                                                                                                                                                   Zhang H., Apfelroth S.D., Hu W., Davis E.C., Bonadio J., Mecham R.P., Ramirez F.; "Structure and expression of fibrillin-2, a component preferentially located in elastic J. Cell Biol. 124:855-863(1994).
             VARIANTS CCA HIS-1.1.14.
MEDLINE=98407789; PubMed=9737771;
                                                  Putnam E.A., Zhang H., Ramirez F., Milewicz D.M.; "Fibrillin-2 (FBN2) mutations result in the Marfan-like disorder, congenital contractural arachnodactyly."; Nat. Genet. 11:456-458(1995).
                                                                                                       VARIANTS CCA TYR-1252 AND SER-1433, MEDLINE=96083599; PubMed=7493032;
                                                                                                                                                                                 MEDLINE-91304567; PubMed-1852206;
Lee B., Godfrey M., Vitale E., Hori H.,
Tsipouras P., Ramirez F., Hollister D.;
                                                                                                                                                                                                                       [2]
SEQUENCE OF 752-1505 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                          Fibrillin
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1994
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                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=94165150;
                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                      Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSCKKGYKGDGYSCIEIDPCADGV----NGGCHEHATCRMTGPGKHKCECKSHYV--GDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KNCMDIDECQRDPLLCRGGVCHNTEGSYRCECPPGHQLSPNISACIDINECELSAHLCPN 1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VDCEPEQLPLDRCLQDN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HNCGKHAVCT--NTAGSFKCSCSPGWIGDGIKCTDLDECSNGTHMCSQHADCKNTMGSYR 1388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PACSVHATCTENNT-----CVCNLNYEGDGTTCTVVDFCKQNNGGCAKVAKCSQKGTQVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---DMKTCVDVNECDLNPNICLSGTCENTKGSFICHCDMGYSGKKGKTGCTDINECEIGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRCVNLIGKYQCACNPGYHSTPDRLFCVDIDECSIMNGGCETFCTNSEGSYECSCQPGFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LMPDQRSCTD1DECEDNPNICDG-GQCTNIPGEY----RCLCYDGFMASE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -MPDCQACPG---GPDTP--CNNRGMCRDL---YTPMGQCLCHTGFNGTACELCWHGRFG
 D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1085
                                                                                                                                                                                                                                                                                                                                                                       Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---VKKKCIYNP----LP---FRRNVE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDCLLMNPTL--GG-------RCDTFTTFDIPGECGSCIFTPKCPLKSK--PK
 Gasner C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel.
(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                            precursor
                                                                                                                                                                                                                                                                                                                                                                                               (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                        29,
33,
40,
                                                                                                                                                                                                                                                                                                                  PubMed=8120105;
                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Francke U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -GOCHPDASCADLYFQDTTVGVFHLRSPLGQYKLTFDKAK 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                        annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence
                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -EGITGSGECLCETGWTAASCDTPTAVFAVC---T
 Maslen
                                                                                                                    AND
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                                                                                                                    VARIANT
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 C.;
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                                                                                                                                                                                                                                                                                                                                                                       Hominidae;
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                                                                                                                                                                                                                                                                  matrices
                                                                                                                                                                                                                                                                              novel microfibrillar
                                                                                                                                                                                                                                                                                                       Sanguineti
                                                                                                                                                                                              M.-G.,
                                                                                                                    ILE.
                                                                                                                                                                      related
                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                 Sarfarazi
                                                                                                                                                                       disorder to
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InterPro: IPR002212; TB.
Pfam; PF00008; ECF; 45.
Pfam; PF000683; TB; 9.
Pfam; PF000683; TB; 9.
PRINTS: PR00010; ECF_CA; 43.
SMART; SM00017; ECF_CA; 43.
SMART; SM00010; ECF_Like;
PROSITE; PS00100; ASX_HYDR
PROSITE; PS00102; ECF_1; PR01186; ECF_2; 3
PROSITE; PS01187; ECF_CA;
EXTRACELIULAR MAILTIX; CALCE
PROSESTE; PS01187; ECF_CA;
EXTRACELIULAR MAILTIX; CALCE
PROSESTE; PS01187; ECF_CA;
PROSESTE; PS0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U03272; AAA18950.1
EMBL; X62009; -; NOT_ANN
PIR; S17063; S17063.
PIR; S31101; S31101.
HSSP; P35555; 1EMN.
MIM; 121050; -
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Godfrey
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InterPro;
InterPro;
InterPro;
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Am. J. Med. Genet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANTS CCA PHE-1141 AND TRP-1252.
MEDLINE=20259236; PubMed=10797416;
Belleh S., Zhou G., Wang M., Der Ka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A single mutation that results in an asp-to-his substitution partial exon skipping in a family with congenital contractual arachnodactyly".

Hum. Genet. 103:22-28(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Two novel fibrillin-2 mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Med. Genet. 92:7-12(2000).

FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS FUNCTION: STRUCTURAL COMPONENT OF CONTAINING MICROFIBRILS REGULATE THAT BINDS CALCIUM, FIBRILLIN-2-CONTAINING MICROFIBRILS REGULATE THE EARLY PROCESS OF ELASTIC FIBER ASSEMBLY.

DISEASE: DEFECTS IN FBN2 ARE THE CAUSE OF CONGENITAL CONTRACTURAL DISEASE: DEFECTIVE (CCA) (ALSO KNOWN AS BEALS SYNDROME). CCA IS PHENOTYPICALLY SIMILAR TO MARFAN SYNDROME, BUT DOES NOT EFFECT THE ADORTA AND THE EYES.

SIMILARITY: CONTAINS 43 CALCIUM-BINDING AND 4 NON-CALCIUM BINDING EGF-LIKE DOMAINS.

SIMILARITY: CONTAINS 7 TGF-BETA BINDING PROTEIN DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TS; PRO0010; EGFBLOOD.
T; SM00179; EGF_CA; 43.
T; SM00001; EGF_like; 3.
TPS; PS00010; ASX_HYDROXYL; 4
TTE; PS00022; EGF_1; 2.
TTE; PS001186; EGF_2; 37.
TTE; PS01187; EGF_CA; 43.
TTE; PS01187; EGF_CA; 43.
TTE; PS01187; EGF_CA; 43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR000152; Asx_hydroxyl.
IPR000561; EGF-like.
IPR001881; EGF_Ca.
IPR001438; EGF_II.
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851
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1.
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POTENTIAL.

POTENTIAL.

POTENTIAL

EGF-LIKE 1

EGF-LIKE 3

EGF-LIKE 5

TGFBP 1.

EGF-LIKE 7

EGF-LIKE 9

EGF-LIKE 9

EGF-LIKE 1

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290; Conser
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MEDLINE=90385285; PubMed=2402639;
COffman C., Harris W., Kintner C.;
"Xotch, the Xenopus homolog of Drosophila Science 249:1438-1441(1990).
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                                                                                                                           European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                   mitted (JUN-1996) to the EMBL/GenBank/DDBJ databases. SUBCELLULAR LOCATION: Type I membrane protein. DEVELOPMENTAL STAGE: EXPRESSED ALMOST UNIFORMLY IN E SIMILARITY: HIGH, WITH OTHER NOTCH-Type PROTEINS. SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS. SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS. SIMILARITY: CONTAINS 6 ANK REPEATS.
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| Interpro; | IPRO01210; ANK. | Interpro; | IPRO0152; Asx_hydroxyl. | Interpro; | IPRO0152; Asx_hydroxyl. | Interpro; | IPR000152; Asx_hydroxyl. | Interpro; | IPR00181; EGF_Ca. | Interpro; | IPR00181; EGF_Like; | Interpro; | IPR00181; EGF_Like; | Interpro; | IPR00181; EGF_Like; | Interpro; | IPR001438; EGF_Like; | Interpro; | IPR00141; EGF_CA; | 23. | Interpro; | IPR00141; EGF_CA; | 23. | Interpro; | IPR00141; EGF_Like; | Interpro; | IPR00141; | INTERPRO; | INTERP
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                                                               TPKDALGRVLQNLTTVAANHGYTKFSKLIQDSGLLSVITD----
                                                                                                                                                                                                    -STSQYFFQLQEHAVRE---
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                    -WPTDKALEALPPEQQDFLFNQDNKDKLKSYLKFHVIRDSKALASDLPR
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21.9%;
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Pred. No. 4.4e-26;
1; Mismatches 457;
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                                          HDHMCLSEVNECNSNPCIHGACHD
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NOTC_DROME
P07207; P041:
01-NOV-1986
01-MAR-2002
MEDLINE=87064624; PubMed=3097517;
Kidd S., Kelley M.R., Young M.W.;
"Sequence of the notch locus of Drosophila melanogaster: of the encoded protein to mammalian clotting and growth f. Mol. Cell. Biol. 6:3094-3108(1986).
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-Oregon R; TISSUE=Embryo;
MEDLINE=66079539; PubMed=9935325;
Wharton K.A., Johansen K.M., Xu T., Artavanis-T
"Nucleotide sequence from the neurogenic locus
"Nucleotide sequence from the neurogenic locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1986 (Rel. 03, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Neurogenic locus Notch protein precursor.
N OR EG:140G11.1 OR EG:163A10.2 OR CG3936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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RA Ballew R.M., Basu A., Auf H. J., Audrews Fidminkoch C., Beduwin D., Ra Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Chandra I., Carley S., Dahlae C., Davenport L.B., Davies P., RA Gherry J.M., Cawley S., Dahlae C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlae C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlae C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlae C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlae C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlae C., Davenport L.B., Davies P., RA Cherry C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Coldek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.L., Houland T.J., Wei M.-H., Ibeqvam C., RA Lasko P., Lei Y., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., L. Lang Y., Lin X., RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.L., RA Merkolov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.L., RA Merkolov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri Y., Reese M.G., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri Y., Reese M.G., RA Merkolov G., Milshina N.V., Moshrefi R., Venter E., Wang A.H., Wang X., RA Walliams S.M., Woodage T., Waristok G.M., Weissenbach J., Ra Mang X., Yang S., Yao Q.A., Zheng L., Yang S., Yao Q.A., Zheng L., Yang S., Taho Q., Zheng L., Ra Mang Y., Thu X., Smith H.O., Zheng G., Zho Q., Zheng L., Ra Maristo
melanogaster.
Mol. Cell. Bio
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MEDLINE-20196011; PubMed=10731137;

Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,

Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E
Dreano S., Gloux S., Lelaure V., Mottler S., Galibert F., Borkova
Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,

Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,

Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F.,

Beinert N., Dowe G., Schaefer U., Jaeckle H., Bucheton A.,

Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,

McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
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STRAIN-Oregon-R;
                                                                                                                                           MEDLINE-87257846; PubMed=3037327; Kelley M.R., Kidd S., Berg R.L., Your "Restriction of P-element insertions melanogaster.";
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                                                        7:1545-1548(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2611 FROM N.A.
PubMed=2981631;
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lons at the
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EMBL; AE003426; AAF45848.2; -.
EMBL; AL035436; CAB37610.1; -.
EMBL; AL035395; CAB37610.1; JOINED.
EMBL; M12175; AAA74496.1; -.
EMBL; M16025; AAA28726.1; -.
PIR; A24420; A24420.
PIR; A24420; A24420.
PIR; A24768; A24768
PIR; A24768; A24768.
                                                                                                                                                                               PRINTS; PRO0010; EGFBLOOD.
PRINTS; PRO1452; NOTCH.
SMART; SM00248; ANK; 4.
SMART; SM00019; EGF_CA; 23.
SMART; SM00001; EGF_like; 13
SMART; SM00004; NL; 2.
                                                                                                                                                                                                                                                                                      InterPro; IPRO02110; ANK.
InterPro; IPR000152; Asx_h;
InterPro; IPR000152; EGF-1:
InterPro; IPR000742; EGF-2:
InterPro; IPR001881; EGF-C:
InterPro; IPR001438; EGF-II
InterPro; IPR001800; Notch
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DOMAIN
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Curr. Biol. 1:120-122(1991).
-i- FUNCTION: NOTCH PROTEIN IS ESSENTIAL FOR PROPER DIFFERENTIATION
                                                           CHAIN
                                                                                                                                                                                                                                                     Pfam; PF00023; ank; 6. Pfam; PF00008; EGF; 36. Pfam; PF00066; notch; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the
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                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harris
                                                                                   fransmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEUROGENIC GENES.
SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE I
SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
SIMILARITY: CONTAINS 6 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Type I membrane protein.

SUBCELLIANEOUS: SEPARATION OF NEUROBLASTS FROM THE ECTODERM INTO THE INNER PART OF EMBRYO IS ONE OF THE FIRST STEPS OF CNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L; M16152; AAB59220.1;
L; M16153; AAB59220.1;
L; M16149; AAB59220.1;
L; M16150; AAB59220.1;
L; M16151; AAB59220.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no resta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M16151; AAA28725.1;
K03508; AAA28725.1;
M13689; AAA28725.1;
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                                                                                                        ; PS50088; ANK_REPEAT; 5.
; PS50297; ANK_REP_REGION; 1; PS00010; ASX_HYDROXYL; 22.
; PS00022; EGF_1; 34.
; PS01186; EGF_2; 28.
; PS01187; EGF_CA; 22.
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                                                                                Signal;
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 2703
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                                                           LOCUS NOTCH PROTEIN
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SCQC--MPGYTGQKCETNIDDCVTNPCGNGGTCIDKVNGYKCVCKVPFTGRDCESKMDPC
                GIDCLLMNPTLGGRCDTFTTFDIPGEC---GSCI----
                                                                                       GLLSVITDSIHTPVTVFWPTDKALEALPPEQQDFLFNQDNKDKLKSYLKFHVIRDSKALA
                                                                                                                   SSDIISTNGVIHVIDKLLSPKNLLI---TPKDALGRVLQNLTTVAANHGYTKFSKLIQDS
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                                                   SDLPRSASWKTLQG-SELSVRCGTG
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23.1%;
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Mammalia; |
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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Genomics 56:70-77(1999).
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Biery N.J., Eldadah Z.A., Moore C.
                                                                                                                                                                                                             "Revised genomic organization
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                                                                                                                  FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICH THAT BINDS CALCIUM. FIBRILLIN-1-CONTAINING MICROFIBRILS LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.

PIM: FORMS INTERMOLECULAR DISULFIDE BONDS EITHER WITH OTHER FORMS INTERMOLECULAR DISULFIDE BONDS OF THE FIBRILLIN-1 MOLECULES OR WITH OTHER COMPONENTS OF THE
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                                                                SIMILARITY: CONTAINS
                                                                                           SIMILARITY:
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Eutheria;
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                                                                             ----ETCFLRYEDEECTLPVVGRHRMDACCCSVGAAWGTEECEECPPRNTPEYEELCPRG
                                                                                                                  ANHGYTKFSKLIQDSGLLSVI----TDSIHTPVTVFWPTDKALEALP---
                                                                                                                                                            --GVCKNGLCVNSKGSF--
                                                                                                                                                                                                                                                                            PFTVFAPLSSSFNHEPRIKDWDQQGLMSQVLRYHVVGCQQLLLDNLKVTTSATTLQGEPV
                                                                                                                                                                                                                                                                                                                      ESTLDPTKTICIETIKGTCWQTIIDGRCEININGAT-----LKSQCCSSLGAAWGSPCT
                                                                                                                                                                                                                                                                                                                                                                                                   PGSFVCTC-PKGFIYKPDLKTCEDIDECESSPCINGVCKNSPGSF
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Pred. No. 7.9e-26;
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01-NOV-1995 (Rel.
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               use by
modified
                                                                                                                                                                                                                                                                                                    Ellisen L.
Smith S.D.
"TAN-1, th
                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1421
                                                                                                                                                                                                                                                                      chromosomal translocations in T Cell 66:649-661(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1373
                                                                                                                                                                                                                                                                                                                                                MEDLINE=91347367; PubMed=1831692;
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTCH1 OR TAN1.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       associated notch
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                                                                                                      SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE PROTEINS SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS. SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS. SIMILARITY: CONTAINS 3 ANK REPEATS.
                                                                                                                                                                SUBCELLULAR LOCATION: Type I membrane TISSUE SPECIFICITY: IN FETAL TISSUES MERAIN STEM AND LUNG. ALSO PRESENT IN MIS FOUND MAINLY IN LYMPHOID TISSUES.
                                                                                                                                                                                                                          FUNCTION: MAY BE IMPORTANT FOR NORMAL LYMPHOCYTE F ALTERED FORM, MAY CONTRIBUTE TO TRANSFORMATION OR IN SOME T-CELL NEOPLASMS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKKGKTGCTDINECEIGAHNCDRHAVCTNTAGSFNCSCSPGWIGDGIKCTDLDECSNGTH
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                                                                                                                                                                                                                                                                                                     the human homolog of the Drosophila notch gene,
                                                                                                                                                                                                                                                                                                                                L.W., Bird J., West D.C.,
requires a license agreement (See http://www.isb-sib.ch/announce,
               non-profit and this st
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. 32, Last sequence update)
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notch protein homolog 1 precursor
protein TAN-1) (Fragment).
               statement
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                                                                                                                                                                                                                                                                                      lymphoblastic
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TRANSMEM
DOMAIN

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Pfam; PF00008; EGF
Pfam; PF00066; note
SMART; SM00248; AN
SMART; SM000179; EGI
SMART; SM00001; EGI
SMART; SM00001; EGI
SMART; SM00001; NL
PROSITE; PS50088;
PROSITE; PS50082;
PROSITE; PS00022;
PROSITE; PS01186;
PROSITE; PS01186;
PROSITE; PS01187;
Differentiation; Nu
Transmembrane; Sig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M73980
HSSP; P00740
MIM; 190198;
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InterPro;
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n; PF00008; EGF; 36.
n; PF00068; EGF; 36.
n; PF00066; notch; 3.
RT; SM00248; ANK; 5.
RT; SM00179; EGF_CA; 22.
RT; SM00011; EGF_Like; 13.
RT; SM00004; NL; 2.
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IPR000152;
IPR000561;
IPR000742;
IPR001881;
IPR000800;
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1IXA.
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 Neurogenesis; Repeat; ignal; Glycoprotein.
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ANK_REP_REGION; 1
ANK_REP_REGION; 1
ASX_HUDROXYL; 20.
EGF_1; 34.
EGF_2; 26.
EGF_CA; 18.
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Asx_hydroxyl.
EGF-like.
EGF_2.
EGF_Ca.
Notch.
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CYTOPLASMIC
EGF-LIKE 2.
EGF-LIKE 3.
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EGF-LIKE 5.
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EGF-LIKE 11.
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EGF-LIKE 11.
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                                                                                  HGACRDSLNGY-KCDCDPGWSGTNCDINNNECESNPCVNGGTCKDMT-SGIVCT
                                                                                                                                                                                                                                   -VRELAGPGPFTVFAPLSSSFNHEPRIKDWDQQGLMSQVLRYHVVGCQQLLLDN
                                                                                                                                                                                                                                                                                                   LCQYDVDECAST -- PCKNGAKCLD-GPNTYTCVCTEGYTG--
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                    -GSC-----IFTPKCPLKSKPKGVK-----KKCIYNPLPFRRNVEGC
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                                                             -SDIGELFLNEQMCRFIHRGLLFDVGVAYGIDCLLMNPTLGGRCDTFTTF
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                                          -C--LNKGTCIDDVAGYKCNCLL
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Pred. No. 7.5e
20; Mismatches
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 -TAGAKGQTCEVDINECVLSPC--
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P98133;
01-OCT-1996
01-OCT-1996
16-OCT-2001
Fibrillin 1
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BOVIN
                                                                                                                                                  microfibrils including the molecular cloning of MAGP-2 J. Biol. Chem. 271:1096-1103(1996).
-:- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE THAT BINDS CALCIUM. FIBRILLIN-1-CONTAINING MICROFIBE LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1150
                                                                                                                                                                                                                                                                 Gibson M.A., Hatzinikolas G., Kumaratilake J.S., Nicholl J.K., Sutherland G.R., Cleary E.G.; "Further characterization of proteins associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1191
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                                                                                                                                                                                                                                                                                                                                        MEDLINE=96132851; PubMed=8557636;
                                                                                                                                                                                                                                                                                                                                                                                                       "Sequence of the coding region of Sequence of the coding region of localization to bovine chromosome Genomics 23:480-485(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                  SIMILARITY:
                                                             MICROFIBRILS.
SIMILARITY: (
                                                                                                          PTM: FORMS INTERMOLECULAR DISULFIDE FIBRILLIN-1 MOLECULES OR WITH OTHER
                                          EGF-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {\tt DNGQCHPDASCADLYFQDTTVGVFHLRSPLGQYKLTFDKAKEACAKEAATIATYNQLSYA}
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                                          DOMAINS
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                     CONTAINS
                                                             CONTAINS
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                  TGF-BETA
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EMBL; L28748; AAA74122.1; -.
HSSP; p3555; lAPJ;
InterPro; IPRO00152; Asx_hydroxyl.
InterPro; IPRO00152; Asx_hydroxyl.
InterPro; IPRO00152; Asx_hydroxyl.
InterPro; IPRO00152; Asx_hydroxyl.
InterPro; IPRO0181; EGF-Like.
InterPro; IPRO0181; EGF-Like.
Pfam; pF00008; EGFBLOOD.
PRINTS; PR00010; EGFBLOOD.
PRINTS; PR00010; EGFLIKE; As.
PROSITE; PS001186; EGF_2; 38.
PROSITE; PS001186; EGF_2; 38.
PROSITE; PS001187; EGF_CA; 45.
Extracellular matrix; Calcium-binding; G1.
Repeat; Signal; Multigene family.
REPEAT 330 390 TGFBP 1.
DOMAIN 81 112 EGF-LIKE 1.
DOMAIN 449 489 EGF-LIKE 1.
DOMAIN 392 446 PRO-RICK 1.
DOMAIN 449 489 EGF-LIKE 1.
DOMAIN 449 489 EGF-LIKE 1.
DOMAIN 449 489 EGF-LIKE 1.
DOMAIN 572 612 EGF-LIKE 1.
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DOMAIN 1113 1154 EGF-LIKE 1.
DOMAIN 1128 1069 EGF-LIKE 1.
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DOMAIN 1155 1196 EGF-LIKE 1.
DOMAIN 1158 1279 EGF-LIKE 1.
DOMAIN 1159 1237 EGF-LIKE 1.
DOMAIN 1168 1321 EGF-LIKE 1.
DOMAIN 1168 1689 EGF-LIKE 2.
DOMAIN 1168 1689 EGF-LIKE 3.
DOMAIN 2016 EGF-LIKE 3.
DOMAIN 2016 EGF-LIKE 3.
DOMAIN 2016 EGF-LIKE 3.
DOMAIN 2016 EGF-LIKE 3.
EGF
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GGF-LIKE 42, C

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                    FWPTDKALEALPPEQQDFLFNQDNKDKLKSYLKFHVIRDSKALASDLPRSASWKTLQGSE 703
                                            MRRSLCYRNYYADNQTCDGELLFNMTKKMCCCSYN
                                                                                                                                      RPNPITVI-
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                                                                                      QCRCPTGYYLNEDTRVCDDVNECETPGICGPGTCYNTVGNYTCICPPDYMQVNGGNNCMD
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                                                                 KLLSPKNLLITPKDALGRVLQNLTTVAANHGYTKFSKLIQDSGLLSVITDSIHTPVTV 643
                                                                                                                                                          -PFTVFAPLSSSFNHEPRIKDWDQQGLMSQVLRYHVVGCQQL--LLDNLKVTTSATTL
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01-NOV-1995 (Rel. 32, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTC_
                                                                                                                                                                                                                Bierkamp C., Campos-Ortega J.A.; "A zebrafish homologue of the Drosophila neurogenic
                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                           Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Euteleostei; Ostariophysi
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                    Neurogenic locus notch NOTCH OR NOTCH1A.
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01-NOV-1995
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                                                                                                                                                                                                                                                                                          SEQUENCE FROM
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                                                                                                                     pattern of transcription during early embryogenesis.";
h. Dev. 43:87-100(1993).
FUNCTION: IMPLICATED IN CELL FATE SPECIFICATIONS DURING EMERYO DEVELOPMENT. MAY BE INVOLVED IN THE FORMATION OF NEURAL PLATE, NOTOCHORD AND BRAIN VESICLES.
           SUBCELLULAR LOCATION: Type I membrane protein.

DEVELOPMENTAL STAGE: EXPRESSED IN ALL CELLS IN PREGASTRULATION

STAGES. DURING GASTRULATION IS DIFFERENTIALLY EXPRESSED,

ACCUMULATING PREDOMINANTLY IN THE PRECHORDAL MESODERM AND

NOTOCHORD. AT THE END OF GASTRULATION, EXPRESSED ALONG THE

ANTERIOR-POSTERIOR AXIS INCLUDING THE DEVELOPING NEURAL PLATE
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DIFFERENTIATING MESODERM. ALSO PRESENT IN THE DEVELOPING
                                                                                                                                                                                                                                                                                        N.A.
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                                                                                                                                                                                                                                                      PubMed=8297791;
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R InterPro; IPRO00742; EGF-2.
R InterPro; IPRO01881; EGF-Ca.
R InterPro; IPRO01881; EGF-Ca.
R InterPro; IPRO01880; Notch.
Pfam; PPO0023; ank; 6.
Pfam; PPO0008; EGF; 36.
Pfam; PPO0008; EGF; 36.
Pfam; PPO0008; EGF; 36.
Pfam; PPO0000; EGFBLOOD.
PRINTS; PRO0010; EGFBLOOD.
PRINTS; PRO1452; NOTCH.
SMART; SM000248; ANK; 5.
SMART; SM000179; EGF-CA; 19.
SMART; SM00001; EGF-11Ke; 16.
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PRINTS: PRO1452; NO
SMART; SM00248; ANN
SMART; SM00179; EGI
SMART; SM00001; EGI
SMART; SM00001; NL,
PROSITE; PS500088;
PROSITE; PS500297;
PROSITE; PS00010; I
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InterPro;
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SIMILARITY: HIGH, WITH OTHER NOTCH-
SIMILARITY: CONTAINS 36 EGF-LIKE DC
SIMILARITY: CONTAINS 3 LIN/NOTCH RE
SIMILARITY: CONTAINS 6 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;; X69088; CAA48831.1; -..; P00740; 1EDM.
;; P00740; 1EDM.
siPro; IPR002110; ANK.
siPro; IPR000152; Asx.hyd
siPro; IPR000561; EGF-lik
siPro; IPR000742; EGF-2.
siPro; IPR001881; EGF-2.
siPro; IPR001438; EGF-II.
siPro; IPR000800; Notch.
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requires
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; ANK_REP_REGION; 1.

**Y HYDROXYL; 23.
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20 POTENTIAL
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EGF_1; 34.
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EGF_2.
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Notch.
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NEUROCENIC LOCUS NEUROCENIC LOCUS NEUROCENIC LOCUS NEXTRACELLULAR (POTE) EGF-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 3.
EGF-LIKE 3.
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EGF-LIKE 6.
EGF-LIKE 7, CALCII EGF-LIKE 9, CALCII EGF-LIKE 10.
EGF-LIKE 11, CALCII EGF-LIKE 11, CALCII EGF-LIKE 12, CALCII EGF-LIKE 13, CALCII EGF-LIKE 14, CALCII EGF-LIKE 14, CALCII EGF-LIKE 15, CALCII EGF-LIKE 16, CALCII EGF-LIKE 17, CALCII EGF-LIKE 18, CALCII EGF-LIKE 19, CALCII EGF-LIKE 11, CALCII EGF-LIKE 11, CALCII EGF-LIKE 11, CALCII EGF-LIKE 12, CALCII EGF-LIKE 20, CALCII EGF-LIKE 21, CALCII EGF-LIKE 22, CALCII EGF-LIKE 23, CALCII EGF-LIKE 23, CALCII EGF-LIKE 24, CALCII EGF-LIKE 25, CALCII EGF-LIKE 26, CALCII EGF-LIKE 26, CALCII EGF-LIKE 27, CALCII EGF-LIKE 2
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CALCIUM-
CALCIUM-
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          EGF-LIKE 28.
EGF-LIKE 29.
EGF-LIKE 30, CALCIUM-BIN
EGF-LIKE 31, CALCIUM-BIN
EGF-LIKE 33, CALCIUM-BIN
EGF-LIKE 33, EGF-LIKE 34.
EGF-LIKE 34.
EGF-LIKE 35.
EGF-LIKE 35.
EGF-LIKE 36.
LIN/NOTCH 1.
LIN/NOTCH 1.
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                                                                                                                                                                                                                                                                                                                     THTCSCLPGETGQTCEHNVDDCTQHACENGGPCIDGINTYNCHCDKHWTGQYCTEDVDE
                                                                                                                                                                                                                                                                                                                                  NRCDNNDTIIVRGECG------KCSQQA-PCPLETKPLRETRKCIYSIY 176
----INGYECVCEPGYSGSMCNINIDDCALNPCHNGGTCIDGV-----NSFTCLCPDGF-
                  DTVFINNEAKVLSSDIISTNGVIHVIDKLLSPKNLLITPKDALGRVLQNLTTVAANHGYT
                                                        PLSSSFNHEPRIKDWDQQGLMSQVLRYHVVGCQQLLLDNLKVTTSATTLQGEPVSISVSQ
                                                                           DGVASFTCDCRPGYTGR--LCETNI-NECLSQPCRNGGTCQDRENAYICTCPKG-----
                                                                                        ASTPCKNGAKCTD-GPNKYTCECTPGFSGIH--CELDINECAS----SP---CHYGVCR
                                                                                                                             ----CDRNAECTQTGPNQAVCNCLPKYTGDGKVCSL-INVCLTNNGGCSPFAFCNYTEQD
                                                                                                                                                           HCICMPGY--EGVFC-QINSDDCASQPCLNGKCIDKINSFHCECPKGFSGSLCQVDVDEC
                                                                                                                                                                              VCVCKAGYTGDGIVCLEIN-----PCL----
                                                                                                                                                                                                  ECSLGANPCEHGGRCLNTKGSFQCKCLQGYEGPRCEMDVNECKSNPCQNDATCLDQIGGF
                                                                                                                                                                                                                    ----AINACETSNGGCSTKA--DCK-------RTTP------
                                                                                                                                                                                                                                        FFCECPHGRTGLLCHLDDACISNPCQKGSNCDTNPVSGKAICTCPPGY--TGSACNQDID
                                                                                                                                                                                                                                                                                CELSPNACQNGGTCHNTIGGFHCVCVNGWTGDDCSENI--DDCASAACSHGATCHDRVAS
                                                                                                                                                                                                                                                                                                                                                             ----GSYLCRCPPEYTGPHCQR-------LYQPCLPSP-----CRSGGTCVQTS-D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.0%; Score 473.5; DB 1; ilarity 20.3%; Pred. No. 3.3e-25; Conservative 123; Mismatches 447;
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RR R X	000 5	DE 07	D D A	RESULT NTC3_M ID N	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	ОУ	Db	0	Db	Qy	Db	Qy	Db	Qy	dd	Qy	Db	Qy	Db	Qy	Db	Qy
Mamma NCBI_ [1] SEQUI	Mus mu Eukary	Neuro	01-NOV-	1: ousi	1386	1185	1349	1129	1297	1073	1250	1015	1199	972	1142	941	1082	896	1022	874	966	846	906	821	856	776	799	726	740	676	707	619
; Sc). Chordata; Craniata; Vertebrata; Euteleosto	16-OCT-2001 (Rel. 40, Last annotation update) Neurogenic locus notch 3 protein.	1997 (Rel. 35, Created)	1 E _MOUSE STANDARD; PRT; 2318 AA.	DSPCLVNPCYNGGTCQPISDAPFYRCSCPANFNGLLCHILDYSFSGGGGR 1435	SKSSAR	SCGSLRCRN-GATCVSGHLSPRCLCAPGFSGHECQTRM 1385	NVVGIVDYGSRANKSEMWDVFCYRMKDVNCTCKAGYVGDGFSCSG	YTGKRCETVFNGCKDTPCKNGGTCAVASNTKHGYICKCQPGYSGSSCEYDSQ 1348	QYKLTFDKAKEACAKEAATIATYNQLSYAQKAKYHLCSAGWLESGRVAYPTTYASQ 1128	GCVCPAGFVGERCEGDVNECLSDPCDPSGSYNCVQLINDFRCECRTG 1296	GVDCEPEQLPLDRCLQD	LVNTYKCSCPRGTQGVHCEIDIDDCSPSVDPLTGEPRCFNGGRCVDRVGGY 1249	GYKGE	EQVDECQPNPCQNGATCTDYLGGYSCECVPGYHGMNCSKEINECLS-QPCQNGGTCID 1198	CKQNNGGCAKVAKCSQKGTQV- 971	ASGWTGIYCDVPSVSCEVAARQQGVSVAVLCRHAGQCVDAGNTHLCRCQAGYTGSYCQ 11	LCETGWTAASCDTPTAVFAVCTPACSVHATCTENNTCVCNLNYEG 940		-CQPRSCSEHGQCDESGEC 895	TCSCPAGFSGINCEINTPDCTESSCFNGGTCVDGISSFSCVCLPGFTGNYCQHDVN 1021	TPMGQCLCHTGENGTACELCWHGREGPD	IDDCEPNPCSNGGVCQDRVNGFVCVCLAGFRGERCAEDIDECVSAPCRNGGNCTDCVNSY 965	MPDCQACPGGY 845	PAGWQGQTCEVDINECVRNPC TNGGVCENLRGGFQC RCNPGFTGALCEND 905	PLKSKPKGVKKKCIYNPLPFRRNVEGCQNLCTVVIQTPRCCHGYF 820	-LNQGSCIDDVAGFKCNCMLPYTGEVCENVLAPCSPRPCKNGGVCRESEDFQSFSCNC 855	FIHRGLLFDVGVAYGIDCLLMNPTLGGRCDTFTTFDIPGECGSCIFTPKC 775	EAGWMGRNCDININECLSNPCVNGGTCKDMTSGYLCTCRAGFSGPNCQMNINECASNPC- 798	KFHVIRDSKALASDLPRSASWKTLQGSEL-SVRCGTGSDIGELFLNEQMCR 725	RDATCLSQHNECSSNP	KESKLIQDSGLLSVITDSIHTPVTVFWPTDKALEALPPEQQDFLFNQDNKDKLKSYL 675

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R InterPro; IPR002110; ANK.
R InterPro; IPR002110; ANK.
R InterPro; IPR000152; Asx_hydroxyl.
R InterPro; IPR000561; EGF-1ike.
R InterPro; IPR000742; EGF_2.
InterPro; IPR001438; EGF_II.
InterPro; IPR001438; EGF_II.
InterPro; IPR000800; Notch.
Pfam; PF00023; ank. 6
                                                                                                                                                                                                                                                                                                                                                                                    pfam; pF00003; ank; 6.

pfam; pF00008; EGF; 34.

pfam; pF00006; notch; 3.

pfam; pF00066; notch; 3.

priwrs; pR00010; EGFBLOOD.

pRINTS; pR001452; NOTCH.

SMART; SM00174; EGF_CA; 19.

SMART; SM00101; EGF_Like; 13.

SMART; SM00104; NL; 3.

SMART; SM00004; NL; 3.

PROSITE; pS50088; ANK_REP_REGIONS PROSITE; pS50097; ANK_REP_REGIONS PROSITE; pS50010; ASX_HYDROXYL PROSITE; pS00101; ASX_HYDROXYL PROSITE; pS001187; EGF_CA; 17.

PROSITE; pS01187; EGF_CA; 17.

PROSITE; pS01187; EGF_CA; 17.

PROSITE; pS01187; EGF_CA; 17.
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Lardelli M., Dalstrand J., Lendahl U.;
"The novel Notch homologue mouse Notch
growth factor-repeats and is avanced."
 TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             growth factor-repeats and is expressed
neuroepithelium.";
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h. Dev. 46:123-136(1994).

FUNCTION: NOTCH 1, 2 AND 3 PLAY A COMBINATIONAL ROLE DURING VARIOUS CELL FATE DECISIONS AND MORPHOLOGICAL MOVEMENTS IN T DEVELOPING CNS AND PROBABLY OTHER REGIONS OF THE EMBRYO.

TISSUE SPECIFICITY: PROLIFERATING NEUROEPITHELIUM.

DEVELOPMENTAL STAGE: CNS DEVELOPMENT S.

SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.

SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
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P00740; 1IXA.
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ANK_REP_REGION;
ASX_HYDROXYL; 18
EGF_1; 33.
EGF_2; 27.
EGF_CA; 17.
   1643
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 CYTOPLASMIC.
PEST-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 3.
EGF-LIKE 5.
EGF-LIKE 5.
EGF-LIKE 5.
EGF-LIKE 11.
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                                                                                                                                   371
                                                                                                                                                   229
                                                                                                                                                                                     180
                                                                                                                                                                                                      280
                                                                                                                                                                                                                                              y Match
Local
YT - -
               YTGDGIVCRGSIYGELPKNPSTSQYFFQLQEHAVRELAGPGPFTVFAPLSSSFNHEPRIK
                                Ď
                                             QTGPNQAVCNCLPKYTGDGKVCSLINVCLTNNGGCSPFAFCNYTEQDQRI
                                                                                                 CGRGYTGPRCETDV--NECLSGPCRNQATC-LDRIGOFTCICMAGF--TGTYCEVDIDEC
                                                                                                        CDVGWRGVKCDMEITTDNC-NGTCHTSANCLLDPDGKASCKCAAGFRGNGTVCTA-INAC
                                                                                                                                           GVNGTGTCQCGLGFNGTAC----ETCTEGKYGIHCDQACSCVH-GRC--SQGPLGDGSCD
                                                                                                                                                                                    KRSVFIGCQPQCVRTIITRACWLASLAHNAKPAPGEVKMCALGTASV--
                                                                                                                                                                                                     QLQPNACHNGGTCFNLLGGHSCVCVNGWTGESCSQNID---
                                                                                                                                                                                                                      EIQKNRCDNNDT
                                                                                  ETS---
                                                                                                                                  PVSGRAICTCPPGFTGGACDQDVDECSIG-----
                                                                                                                                                                                                                                      ol Similarity
255; Conser
                                 PDGYECRCAEGE
-GIRCESQV-DECRSQP--CRYGGKCLDLVDKYLCRCPPGT----
                                                                          NGGCSTKADCKRTTPGNRVCVCKAGYTGDGIVC-LEINPCLENHGGCDRNAECT
                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                    ATCHDRVASFYC-----
                                                                                                                                                                                                                                                                       EG
                                                                -CKDRVNGFS-CTCPSGFSGS--MCQLDVDECAST--PCRNGAKCV
                                                                                                                                                                                                                                             22
                                                                                                                                                                                                                                             .0%;
                                                                                                                                                                                                                                     101;
                                                                                                                                                                                                              - IIVRGECGK-CSQQAPCPLETKPLRETRKCIYSIYFMG
: | | | : | | | : : | |
                                                                                                                                                                                                                                     Score 473; DB Pred. No. 3.3e
                                                                                                                                                                                                                                                                       SIMILARITY
                                                                                                                                                                    ACPMGKTGLLCHLDDACVSNPCHEDAICDTN
                                                                                                                                                                                                                                             DB 1;
.3e-25;
                                                                                                                                  -ANPCEHLGRCVNTQGSF----LCQ
                               -CHHGRCVDGIASFSCACAPG
                                                                                                                                                                                                                                                    Length 2318;
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                     -----DCATAVCFHG
TGVNCEVNID
                                                                                                                                                                                                                                     420;
                                               CTCKPD
                                                                                                                                                                                    WD
                                                                                                                                                                                                                                     Gaps
                                                                                                                                  419
                                               451
                                                                                395
                                                                                                                                                                                                    327
                                                                                                                                                                                                                     179
                                                                                                  474
                                                                                                                  339
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RESULT NTCL. RAS ID OF COLOR O
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                                                                                                                                                    Rattus norvegicus (Re
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
NCBI_TaxID=10116;
                                                                                                                                                                                                                                              NTC1_RAT
Q07008;
01-NOV-1995
15-JUL-1999
16-OCT-2001
Neurogenic Lo
SEQUENCE FROM N.A.
TISSUB-Schwann cell;
TISSUB-Schwann cell;
MEDLINE-92111383; PubMed=1764995;
Weinmaster G., Roberts V.J., Lemk
"A homolog of Drosophila Notch ex
development.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTFDKAKEACAKEAATIATYNQLSYAQKAKYHLCSAGWLESGRV----AYPTTYASQKCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ECPAGYAGD --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VRLEQLCQEGGKCIDKGRSHYCVCPEGRTGSHCEHEVDPCTAQPCQHGGTCRGYMGGYVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANVVGIVDYGSRA-NKSEMWDVFCYR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGFTGS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGGTCVDGVSSFSCLCRPGYTGT-HCQYEADPC---FSRPCLHGGICNPTHPG-FECTCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KVAKCSQKGTQVSCSCKKGYKGDGYSCIEIDPCADGVNGGCHEHATCRMTGPGKHKCECK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -PGNFRCICHRGYTGPFCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKCIYNPLPFRRNVEGCQNLCTVVIQTPRCCHGYFMPDCQACPGGPDTPCNNRGMCRDLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIHRGLLFDVGVAYGIDCLLMNPTLGGRCDTFTTFDIPGECGSCIFTPKCPLKSKPKGVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNKDKLKSYLKFHVIRDSKALASDLPRSASWKTLQGSELSVRCGTGSDIGELFLNEQMCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLIQDSGLLSVITDSIHTPVT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NNEAKVLSSDIISTNGVIHVIDKLLSPKNL--LITPKDALGRVLQNLTTVAANHGYTKFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DCASNPCTFGVCRDGINRYDCV-CQPGFTGPLCNVEINECASSPCGEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DWDQQ----GLMSQ-VLRYHVVGCQQLL---LDNLKVTTSATTLQGEPVSISVSQDTVFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -QCLCHTGFNGTACELCWHGRFGPDCQPRSCSEHGQCDEGITGSGECLCETGWTAA
                                                                                                                                                                                                                                                                i (Rel. 32, Created)
(Rel. 38, Last sequence update)
(Rel. 40, Last annotation update)
Locus notch homolog protein 1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --00---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -PDRLTV--CS-
                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCEDNI
                                                                                                                                                                              ; (Rat).
Da; Chordata;
La; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -QNPVDWCSQAPCQNGGRC

    PCAHKPCSHGVCHDAPGGFRCVCEPGWSGPRCSQSLAPD

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GHQCEVLSPCTPSLCEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -GTCTDHVASFTCACPPGY--GGFHCE-IDLPDCSPSSCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -QDIDDCDPNPCLHGGSCQDGV
                                               Lemke
                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VQTGAYCICPPGW-
                       expressed
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                                               G
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                       during
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                       mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -ANH
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                                                                                                                                                                                   Rattus
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Devc.
[2]

REVISIONS 1.
A Weinmaster G.;
AL Submitted (APR-195.
CC -!- FUNCTION: REQUIREL
CC OF TISSUES.
CC -!- SUBCELLULAR LOCATION: Ty.
-!- DEVELOPMENTAL STAGE: IN
DAYS 12 AND 14 AND DEC

"I.T.
"TY: HIGH, V
"ONTA"
      InterPro: IPRO02110; ANK.
InterPro: IPRO00152; Asx_hydroxyl.
InterPro: IPRO00561; EGF-like.
InterPro: IPRO00561; EGF-like.
InterPro: IPRO00742; EGF_Ca.
InterPro: IPRO001881; EGF_Ca.
InterPro: IPRO002049; Laminin_EGF.
InterPro: IPRO002049; Laminin_EGF.
InterPro: IPRO00800; Notch.
Pfam; PF00006; notch; 3.
Pfam; PF00006; notch; 3.
Pfam; PF00010; EGFEAMININ.
PRINTS; PR00011; EGFEAMININ.
PRINTS; PR00011; EGFEAMININ.
PRINTS; PR00011; EGFEAMININ.
PRINTS; SM00179; EGF_CA; 25.
SMART; SM00104; ANK; 5.
SMART; SM00104; ANK; 5.
SMART; SM00004; NC: 2.
PROSITE; PS5008; ANK_REPEAT; 4.
PROSITE; PS50018; ANK_REPEAT; 4.
PROSITE; PS501187; EGF_CA; 21.
Differentiation; Neurogenesis; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by centities requires a license agreement /c^-
   Transmembrane;
SIGNAL 19
CHAIN 19
CHAIN 19
DOMAIN 1724
DOMAIN 20
DOMAIN 174
DOMAIN 174
DOMAIN 174
DOMAIN 174
DOMAIN 174
DOMAIN 257
DOMAIN 257
DOMAIN 257
DOMAIN 257
DOMAIN 257
DOMAIN 335
DOMAIN 372
DOMAIN 452
DOMAIN 452
DOMAIN 452
DOMAIN 452
DOMAIN 456
DOMAIN 568
DOMAIN 568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Development 113:199-205(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DAYS 12 AND 14 AND DECREASE RAPIDLY TO MURADULT.
SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE F
SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS
SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
SIMILARITY: CONTAINS 5 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                 Signal
                                                                                                                                                                                                                                                                                                                                               Neurogenesis; Repeat; ignal; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OCATION: Type I membrane protein
STAGE: IN THE EMBRYO, HIGHEST LI
4 AND DECREASE RAPIDLY TO MUCH LI
     the
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CYTOPLASMIC (POTENTIAL).

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EGF-LIKE 2.

EGF-LIKE 5.

EGF-LIKE 5.

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EGF-LIKE 6.

EGF-LIKE 7.

CALCIUM-BINDING
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CALCIUM-BINDING
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    [1]
SEQUENCE FROM |
TISSUE=Embryo;
                                                                                                                                                    Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RGIDVTLLCQHGGLCVDEEDKHYCHCQAGYTGS--YCEDE--
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                                                                                                                                                            Chordata;
Rodentia;
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                                                                                                                                                        Craniata; Ver
Sciurognathi;
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                                                                                                                                                                                                    Vertebrata;
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                                                                                                                                                                Muridae;
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                                                                                                                                                                Murinae;
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InterPIC,
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                    AREDLINE 93048835; PubMed-1425352;

X MEDLINE-93048835; PubMed-1425352;

A Franco del Amo F., Smith D.E., Swiatek P.J., Gendron-Wag A Greenspan R.J., McMahon A.P., Gridley T.;

Pagreession pattern of Motch, a mouse homolog of Drosoph T suggests an important role in early postimplantation mou development.";

Development 115:737-744(1992).

C -!- SUBCELLULAR LOCATION: Type I membrane protein.

C -!- SUBCELLULAR LOCATION: Type I membrane protein.

C -!- SUBCELLULAR STAGE: EXPRESSED ALMOST UNIFORMLY IN ECHICA STAGE: EXPRESSED ALMOST UNIFORMLY IN ECHICA SIMILARITY: CONTAINS 3 LIM/NOTCH REPEATS.

C -!- SIMILARITY: CONTAINS 3 LIM/NOTCH REPEATS.

C -!- SIMILARITY: CONTAINS 5 ANK REPEATS.
                Transmembrane:
SIGNAL 19
CHAIN 19
DOMAIN 19
TRANSMEM 1726
DOMAIN 1747
DOMAIN 102
DOMAIN 102
DOMAIN 102
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DOMAIN 1140
DOMAIN 117
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DOMAIN 257
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InterPro;
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MGI:97363;
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; IPR000152; Asx_hydroxyl.
; IPR000561; EGF-like.
; IPR000742; EGF_2.
; IPR001881; EGF_Ca.
; IPR001438; EGF_II.
; IPR000800; Notch.
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and this statement is not removed
requires a license agreement (See
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18 POTENTIAL.
19 POTENTIAL.
1 NEUROGENIC LOCU.
1 NEUROGENIC LOCU.
2 EGF-LIKE 1.
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CMDKIHEFQCQCPKGFNGHLCQYDVDECASTPCKNGAKCLDGPNTYTCVCTEGYTGTH--
                                                                                SCKCAAGFRGNGTVCTA-INACETSNGGCSTKADCKRTTPGNRVCVCKAGYTGDGIVC-L
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                                                                      {\tt ICTCPSGY--TGPACSQDVDECDLGANRCEHAGKCLNTL-GSFECQCLQGYTGPG}
                                                                                                         CASAACFQGATCHDRVASFYCECPHGRTGLLCHLKHAC - - ISNPCNEGSNCDTNPVNGKR
                                                                                                                                              YNCRCPPEVTGQYCTEDVDECQLMPNACQNAGTCHNTHGGYNCVCVNGWTGEDCSENIDD
                                                                                                                                                                                 PSPCQNGATCRPTGDTTHECAC-LPGFAGQNCEENVDDCPG--NNCKNGGACV-DGVN-T
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                                                                                                                                                                                                                   NECSQNPGLCRHG--GHCHNEIGSYRCACCATHTGPHCEL
                                                                                                                                                                                                                                    NRCDNNDTIIVRGECGKCSQQ-----APCPLETKPLRETRKCIYSIYFMGKRSVFIGCQ
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                                 . 7%;
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Pred. No. 3.7e<sup>o</sup>
04; Mismatches
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                                                      _MOUSE | STANDARD; PRT; 1964 AA. P31695; Q62389; O1_JUL-1993 (Rel. 26, Created) O1-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Neurogenic locus notch homolog protein 4 precursor
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                                                                                                                                                                                                                 E--RCEGDVNECL
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                                                                                                                                                                                                                                                                                                         YPTTYASOKCGANVVGI----VDYGSRANKSEMWDVFCY-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              RWC--DSAPCKNGGRCWQTNTQYHCECRSGWTGVNCDVLSVSC-EVAAQKRGIDVTLLCQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \verb|FTCLCPPGFTGSYCQYD--VNECDSRPCLHGGTCQDSYGTYKCTCPQGY--TGLNCQNLV|\\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QNGANCTDCVDSYT----CTCPVGFNGIHCE----NNTPDCTESSCFNGGTCVDGI-NS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNRGMCRDL---YTPMGQCLCHTGFNGTACELCWHGRFGPDCQPRSCSEHGQCDEGITGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CKNSGVCKESEDYESFSCVCPTGWQGQTCEVDINECVKSPC---RHGASCQNTNGSYRCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {\tt TCREGFSGPNCQTNINECASNPCLNQGTCIDDVAGYKCNCPLPYTGATCEVVLAPCATSP}
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                                                                                                                                                                                                                                                                                                                                                                                                   HGGLCVDEG
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                                                                                                                                                                                                                                                                              -PRGTQGVHCEINVDDCHPPLDPASRSPK
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protein INT-3).
NOTCH4 OR INT3 OR INT
Mus musculus (Mouse).
Eukaryota; Metazoa; C

OR INT-3.

Chordata;

Craniata;

Vertebrata;

Euteleostomi;

(Transforming

```
pfam; PF00023; ank; 6.

pfam; PF00008; EGF; 27.

pfam; PF00008; EGF; 27.

pfam; PF00066; notch; 2.

prints; Pr001415; ANKKRIN.

prints; PR01415; ANKKRIN.

prints; PR01415; NOTCH.

SMART; SM001452; NOTCH.

SMART; SM00179; EGF_CA; 11.

SMART; SM00001; EGF_1ike; 15.

SMART; SM00001; EGF_1ike; 15.

SMART; SM00001; AL; 21.

SMART; SM00001; AL; 28.

PROSITE; PS50088; ANK_REPEAT; 5.

PROSITE; PS50010; ASK_HYDROXYL; 11.

PROSITE; PS001187; EGF_1; 28.

PROSITE; PS01186; EGF_2; 21.

PROSITE; PS01187; EGF_CA; 9.

Differentiation; Neurogenesis; Repeat Glycoprotein; Proto-oncogene; ANK_rep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M80456; AAB3837
EMBL; U43691; AAC5263
PIR; A3072; TVMVT3.
HSSP; P08709; 1BF9.
MGD; MGI:107471; Notcl
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[3]
     TRANSMEM
DOMAIN
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InterPro;
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InterPro;
InterPro;
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between
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MEDLINE-96281668; PubMed-8681805;
Uyttendaele H., Marazzi G., Wu G., Yan Q
"Notch4/int-3, a mammary proto-oncogene,
cell-specific mammalian Notch gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Development 122:2251-2259(1996).

-i- SUBCELLULAR LOCATION: Type I membrane protein.
-i- DISEASE: ACTIVATED INT-3 TRANSFORMS MAMMARY EF.
-i- SIMILARITY: CONTAINS 29 EGF-LIKE DOMAINS.
-i- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
-i- SIMILARITY: CONTAINS 5 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVISIONS, SEQUENCE FROM N.A.
MEDLINE=97294599; PubMed=9150355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Robbins J., Blondel B.J., Gallahan D., Cal
"Mouse mammary tumor gene int-3: a member
transforms mammary epithelial cells.";
J. Virol. 66:2594-2599(1992).
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Robbine
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                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ahan D., Caliahan R.;
mouse mammary tumor associated
NOTCH gene family (NOTCH4).";
gene 14:1883-1890(1997).
                                                                                                                                                                                                                                                                                                                                                                             5; IPR002110; ANK.
5; IPR000152; Asx_hydroxyl.
5; IPR000561; EGF-1ke.
5; IPR000742; EGF_2.
6; IPR001881; EGF_Ca.
6; IPR001438; EGF_II.
7; IPR000800; Notch.
                                     1; Proto-oncogene;

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21 1964 N

21 1443 E
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AAC52630.1; -.
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is; Repeat; EGF-like domain; e; ANK repeat; Signal.
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NEUROGENIC LOCUS NOTCH HOMC EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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                                                                                  EGF-like domain;
at; Signal.
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PLTGSTLCICQPGYSGS--TCHQDLDECQMAQQGFSPCEHGGSC:
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TGSRCEADHNECLSQPCHPGSTCLDLLATFHCLCPPGLEGRLCEVEVNECTSN--PCLNQ
                         TG----
                                                                                              DDCAAATCAPGSTC-IDRVGSFSCLCPPG--RTGLLCHLEDMCLSQ--PCHVNAQCS-TN
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21.8%;
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Pred. No. 1.1e
95; Mismatches
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                     -----DGKVCSL-INVCLTNNGGCSPF
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1.1e-22;
hes 347;
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RESULT 15

TENX_HUMAN STANDARD; PRT; ***.

ID TENX_HUMAN STANDARD; PRT; ***.

AC P22105; P78530; P78531; Q08424; Q9UMG7;

DT 01-AUG-1991 (Rel. 19, Created)

DT 16-CCT-2001 (Rel. 40, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Tenascin-X precursor (TN-X) (Hexabrachion-like).

AN TNXB OR TNX OR XB OR HXBL.
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                                                                                          Rowen L.,
Banta A.,
                                                              "Sequence
locus.";
                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; MOBI_TaxID=9606;
                                                                                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                         952
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                                                                          FROM N.A.

Dankers C., Baskin D., Faust J., I
Schwartzell S., Smith T.M., Spies
determination of 300 kilobases of
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                                                                                                                                                           Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLCQDNMNPCEPNPCHHGSTCVPQPSGYVCQ
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                                                                          es T., Hood L
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[2]
SEQUENCE OF 1-747 A
TISSUE=Leukocyte;
MEDLINE=93300909; F

AND

1687-1944 FROM the

N . A .

ço

EMBL/GenBank/DDBJ

PubMed=7686164;

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MEDLINE-89367293; PubMed=2475872;

A MOTEL Y. Bristow J., Gitelman S.E., Miller W.L.;

T "Transcript encoded on the opposite strand of the human :

hydroxylase/complement component C4 gene locus.";

proc. Natl. Acad. Sci. U.S.A. 86:6582-6586(1989).

-i-FUNCTION: APPEARS TO MEDIATE INTERACTIONS BETWEEN CEL
EXTRACELLULAR MATRIX. SUBSTRATE-ADHESION MOLECULE THA
INHIBIT CELL MIGRATION. MAY PLAY A ROLE IN SUPPORTING
OF EPITHELIAL TUNGRS.
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or send an em
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TISSUE=Adrenal gland;
MEDLINE=96015044; PubMed=8530023;
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J. Cell Biol. 122:265-278(1993).
                                                  InterPro;
InterPro;
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EMBL;
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MEDLLNE=97081760; PubMed=923003;
Speek M., Barry F., Miller W.L.;
Speek M., Barry F., Miller W.L.;
"Alternate promoters and alternate splicing of gene with 5' and 3' ends buried in other genes.
Hum. Mol. Genet. 5:1749-1758(1996).
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ENLIGARITY: CONTAINS 19 EGF-LIKE DOMAINS.

SIMILARITY: CONTAINS 32 FIBRONECTIN TYPE III-LIKE DOMAINS.

SIMILARITY: CONTAINS 32 FIBRONECTIN TYPE III-LIKE DOMAINS.

SIMILARITY: CONTAINS 3 DOMAIN RELATED TO THE C-TERMINAL PART THE BETA AND GAMMA CHAINS OF FIBRINGEN.

CAUTION: THERE ARE TWO GENES FOR TN-X: TNXA AND TNXB. TNXA I A PARTIAL GENE WHICH CAN SOMETIME RECOMBINE WITH TNXB.
erPro; IPR000561; EGF-like.
erPro; IPR003961; FN_III.
srPro; IPR002181; Fibrinogen_C.
erPro; IPR002049; Laminin_EGF.
i; PF00147; fibrinogen_C; 1.
i; PF00041; fn3; 6.
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SUBCELLULAR LOCATION: Extracellular matrix.
ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; XB (SHOWN HERE) A
XB-SHORT; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN FETAL ADRENAL, IN FI
TESTIS, FETAL SMOOTH, STRAATED AND CARDIAC MUSCLE. XB-SHORT
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SM000181; EGF; 8.

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SM00186; FBG; 1.

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KCECKS : QCVCVE	INGGCAKVAKC	LCETGWTA: :::	CNNRGMCRD	VKKKCIYNP- : : VDGRCVCNPG	RGLLFDVGV SGEDCGV	KLKSYL	TKFSKLI	QDTVFINN	1	APLSSSFI	YTEQDQRI : KDGR-	INPCLENH : MRSCPR	KASCKCAAG : QGVCVCRAG	GIHCDQACSC : PDDCNDQGRC	EV	ore 435; ed. No. 3 Mismatch	-LINKED (C-LINKED (CISSING (IN -> GEQG (IN -> I
YVGDGV : FRGP	SQKG : RGRG	ASCDT	LYTPM	FTGED	-AYG : RSCP		IQDSGLLSV : -DDCGVRSC	EAKVLS		FNHEPRIKI	ICTCKPDYTGDGI 	LENHGGCDRNAE : PRGCSQRGR	FRGNG : FSG	VHGRCS	KMCALGT/ : : /RTLCSL1	DB 1; .8e-22 es 31	(GLCNAC) (GLCNAC) (IN ISOFORM G (IN REF. 2 G (IN REF. 3 AN IN REF. 3 AN 7C12C65C647C
VDCEPEQL ; PDCAIQTC	RCVQGVCLC	AVFAVC	LCHTG : VCEDG	RRN 	IDCLLMNPT	KALASE : RGRG	ITD- PGDC	SDIISTNG	PWD	IKDWDQQGLMSQV	ດ <	CTQTG	CTAINA : : CSQ-RS	QGPLGDG	ASVWDGV : HGVFD	Lengt; ; 8; Ind	XB-
.PLDRCLQ ; !PGDCR	CKKGYKG CHVGYGG	TPACSVH	FNGTACE:: :: - YSGEDC-	CQ : CRGH	LGGRC GRGRC	LPRSASW	SIHTP	GVIHVID		LR	CRGSIYG	PNQAVCN -ENGRCV	CETSNGG	SCDCDVG CFPG	VNGTGTCQ -LSRCTCS	h 4289; els 35	(POTENTI (POTENTI: SHORT).
DNGQC : RGRGEC	DGYSC : EDC	VHATCTE GRGRC-E	CLCWHG	NLCTVVI : GLCEDGV	DTFTTF:: :: :ESGRCM	ASWKTLQG	PVTVFW GRCVCW	KLLSP	CGE	YHVVGC	ELPKN	NCLPKY CNPGY	GCSTKA	GWRGVK : GYTGPS	OCGLGE : CEPGW	4; Ga	TAL).
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US-08-185-432-18 Sequence 18, Application US/08185432 Patent No. 575652 GENERAL INFORMATION: APPLICANT: Artavanis-Tsakonas, Spyridon APPLICANT: Diederich, Robert J. APPLICANT: Diederich, Robert J. APPLICANT: Matsuno, Kenji TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, TITLE OF INVENTION: ANTHODIES, AND RELATED METHODS NUMBER OF SEQUENCES: 23 CORRESPONDENCE ADDRESS: ADDRESSE: PENNIE & EDMONDS STREET: 1155 Avenue of the Americas CITY: New YORK STATE: New YORK STATE: New YORK COUNTRY: U.S.A. 2IP: 10036-2711 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Ploppy disk COMPUTER READABLE FORM: APPLICATION NUMBER: 15,872 APPLICATION NUMBER: US/08/185,432 FILING DATE: 21-JAN-1994 CLASSIFICATION NUMBER: 18,872 REFERENCE/DOCKET NUMBER: 7326-006 TELEFAX: (212) 869-8864/9741 TELECHONE: (212) 869-8864/9741 TELECHONE: C122 790-9090 TELEFAX: (212) 869-8864/9741 TELECOMMUNICATION INFORMATION: SEQUENCE CHARACTERISTICS: LENGTH: 2523 amino acids TYPE: maino acid TYPE: maino acid TYPE: minon acid TYPE: minon acid TYPE: Unknown US-08-185-432-18	28 341.5 4.3 1055 4 US-09-214-278-2 29 341.5 4.3 1212 4 US-09-214-278-3 30 341.5 4.3 1227 3 US-08-611-729A-8 31 339.5 4.3 1248 4 US-08-802-046-6 32 337.5 4.3 3075 2 US-08-125-077-5 34 31 4.2 1238 5 PCT-US95-11644-2 35 325 4.1 1219 5 PCT-US95-11644-2 36 324.5 4.1 1810 5 PCT-US95-11644-2 37 322 4.1 1525 3 US-09-194-647-2 38 322 4.1 1525 4 US-09-540-245A-2 40 279 3.5 713 3 US-08-972-855-5 41 278.5 3.5 833 1 US-08-264-534-6 42 276.5 3.5 833 1 US-08-083-590A-2 44 276.5 3.5 833 1 US-08-346-126-6 45 276.5 3.5 833 2 US-08-346-126-6
AND COMPOSITIONS	Sequence 2, Appli Sequence 3, Appli Sequence 6, Appli Sequence 5, Appli Sequence 5, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 5, Appli Sequence 6, Appli

Query Match
Best Local Similarity
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6.2%; 131;

Score 486; DB 1 Pred. No. 8e-31; Mismatches

DB 1; Length 2523;

Indels 486;

Gaps

93;

974	ACSVHATCTENNTCVCNLNYEGDGITC-TVVDFCKQNNGGCAKVAKCSQKGTQVSCS	Qy 919	_
1027	o -	Db 976	_
918	GTACELCWHGREGPDCQPRSCSEHGQCDEGITGSGECLCETGWTAASCDTPTAVFAVCTP	Qy 859	_
975	CSDGINMFFCN-CPAGFRGPKCEEDINECASNPCKNGANCTDCVNS	Db 921	_
858	-	Оу 818	_
920	NGATCQNTNGSYKCNCKPGYTGRNCEMDIDDC	Db 879	_
817	KCPLKSKPKGVKKKCIYNPLPFRRN	Qy 774	\sim
878	PYTGAICEAVLAPCAGSPCKNGGRCKESEDFETFSCECPPGWQGQTCEIDMNECVNRPCR	Db 819	-
773		Qy 746	_
818	GGTCKDMTGAYICT-CKAGFSGPNCQTNINECSSNPCLNHGTCIDDVAGYKCNCML	Db 764	п
745	SASWKTLQGSELSVRCGTGSDIGELFLNEQMCRF	Qy 693	0
763	GVNGYKCDCEA	Db 732	н
692	PYTYFWPTDKALEALPPEQQDFLENQDNKDKLKSYLKFHV	Qy 640	2
731	NPCRNGGTCKD	Db 684	н
639	RVLONLTTVAANHGYTKFSKL	Qy 596	2
683	TCPKGTTGVNCETKIDDCASNLCDNGKCIDKIDGYECTCEPGYTGKLCNININECDS	Db 627	п
595	SVSQDTVFINNEAKVLSSDIISTNGVIHVIDKLLSPKNLLI	Qy 555	0
626	NECIPDPCHYGTCKDGIATFTCLCRPGYTGRLCDNDINECLSKPCLNGGQCTDRENGYIC	Db 567	ь
554	EPRIKDWDQQGLMSQVLRYHVVGCQQLLLDNLKVTTSATTLQGEPVSI	Qy 507	Ω
566	KINEFRCDCPTGFSGNLCQHDFDECTSTPCKNGAKCLDGPNSYTCQCTEGFTGRHCEQDI	Db 507	ь
506	TVFAPLSSSFNH	Qy 472	0
506	NECLSNPCQNDSTC-LDQIGEFQCICMPGYEGLYCETNI-DECASNPCLHNGKCID	Db 453	\Box
471	VCLTNNGGCSPFAFCNYTEQDQRICTCKPDYTGDGIVCRGSIYGELPKNP	Qy 421	Ω
452	ACNNDVDECSLGANPCEHGGRCTNTLGSFQCNCPQGYAGPRCEIDV	Db 404	
420	CLENHGGCDRNAECTQT-GPNQAVCNCLPKYTGDGKVCSL-I	QУ 369	O
403	-HDRVASFYCECPHGRTGLLCHLDNACISNPCNEGSNCD-TNPVNGKAICTCPPGY	Db 350	ы
368	RGNGTVCTAINACETSNGGCSTKADCKRTTPGNRVCVCKAGY	Оу 313	Ю
349	DVDECQLMPNACQNGGTCHNTYGGYNCVCVNGWTGEDCSENIDDCANAACHSGATC	Db 294	ь
312	Ľ	Qy 264	Ø
293	QTDDTSYDCTCLPGFSGQNCEENIDDCPSNNCRNGGTCVDGVNTYNCQCPPDWTGQYCTE	Db 234	D
263	DQAC	Оу 238	0
233	SPCLNG-GTCR	Db 190	D
237	AKPAPGEVKMCALGTASVWDGVNGTGTCQ	Qy 190	Ø
189	SCQQADPCASNPCANGGKCLPFEIQYICKCPPGFHGATCKQDINECSQNPCK	Db 138	D
189		Oy 151	0
137	FICHCPVGFTDKVCLTPVDNACVNNPCRNGGTCELLNSVTE-YKCRCPPGWTGD	Db 85	D
150	VNEAPINYTNVATDKGVIHGLEKVLEIQKNRCDNNDTIIVRGECG	Qy 105	Ø

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INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 2556 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-083-590A-20
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US-08-083-590A-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20, Application US/08083590A Patent No. 5786158
                                                                                                                           Query Match
Best Local Similarity
Matches 269; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/083
FILING DATE: 25-JUN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Lesile
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869864/9741
TELEFX: 66141 PENNIE
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TITLE OF INVENTION: Therapeutic And Diagnostic Methods
TITLE OF INVENTION: And Compositions Based On No. 5786158ch Proteins And
TITLE OF INVENTION: Nucleic Acids
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FROM PC COMPATING SYSTEM: PC-DOS/MS-DOS
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                                           ENIDDCPGNNCKNG-----GACVDGVNTYNCPCPPEWTGQYCTEDVDECQLMPNACQNG 309
                                                                                  EKVLEIQKNRCDNNDTIIVRGEC--GKCSQQAPCPLE-----TKPLRETR------
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1155 Avenue of the Americas
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                                                                                                                              Conservative 120; Mismatches 445;
    -KCIYSIYFMGKRSVFIGCQPQCVRTI---ITRACWLASLAHNAK-----
                                                                                                                                               6.1%; Score 480.5; DB 1
21.7%; Pred. No. 2.3e-30;
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                                                                                                                                                                       DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DIPGEC---GSC----IFTPKCPLKSKPKGVK------KKCIYNPLPFRRNVEGC
                                              --SPCQNGATCTDY-----LGGYSCKCVAGYHGVNCSEEIDECLS------
                                                                                                                                                                                                          NLNYEGDGITC-TVVDFCKONNGGCAKVAKCSQKGTQVSCSCKKGYKG-----DGYSCIE
                                                                                                                                                                                                                                                                     CSEHGOCDEGITGSGECLCETGWTAASCDTPTAVFAVC-TPACSVHATCTEN---NTCVC
                                                                                                                                                                                                                                                                                                       DCLPGFRGTFCEEDINECASDPCRNGANCTDCVDSYTCTCPAGFSGIHCENNTPDCTESS
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                                                                              DNGQCHPDASCADLYFQDTTVGVFHLRSPLGQYKLTFDKAKEACAKEAATIATYNQLSYA
                                                                                                                                                                                                                                          CFNGGTCVDGI-NSFTCLCPPGFTGSYCQ---HVVNECDSRPCLLGGTCQDGRGLHRCTC
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                                                                                                             VAAQRQGVDVARLCQHGGLCVDAG-NTHHCRCQAGYTGSYCEDLVDECSP----
                                                                                                                                  IDPCADGVNGG--CHEHATCRMTGPGKHKCECKSHYVG----DGVD-CEPEQLPLDRCLQ
                                                                                                                                                                           \verb"PQGYTGP--NCQNLVHWC--DSSPCKNGGKCWQTHTQYRCECPSGWTGLYCDVPSVSC-E"
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION: 424
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: 08/083,590
APPLICATION NUMBER: 25-JUN-1993
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
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REFERENCE/DOCKET NUMBER: 73
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869864/9741
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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LENGTH: 2556 amino acids
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AVENTION: Therapeutic And Diagnostic Methods
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AVENTION: Nucleic Acids
SEQUENCES: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQDFLFNQDNKDKLKSYLKFHV------IRDSKALASDLPRSASWKTLQGSELSVR 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KDALGRVLQNLTTVAANHGYTKFSKLIQDSGLLSVITDSIHTPVTVFWPTDKALEALPPE 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKVTTSATTLQGEPVSISVSQDTVFINNEAKVLSSDIISTNGVIHVIDKLLSPKNLLITP 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAYLCFCLKGTTGP------CASSPCDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HA-----VRELAGPGPFTVFAPLSSSFNHEPRIKDWDQQGLMSQVLRYHVVGCQQLLLDN 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGGCSPFAFCNYTEODORI----CTCKPDYTGDGIVCRGSIYGELPKNPSTSQYFFQLQE 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FTGH--LCQYDVDECAST--PCKNGAKCLD-GPNTYTCVCTEGYTG-----THCEVD 566
                                                                                                                                                                                                                                                                                                                                                                                                     CSEHGQCDEGITGSGECLCETGWTAASCDTPTAVFAVC-TPACSVHATCTEN---NTCVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QN\hbox{-----}THGGYRCHCQAGYSGRNCETDIDDCRPNPCHNGGSCTDGINTAF--C}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----HGACRDSLNGY-KCDCDPGWSGTNCDINNNECESNPCVNGGTCKDMT-SGIVCT 778
                                    WDVFCY-----RMKDVNCTCKAGYVGDGFSCSGNLLQVL 1183
                                                                                                                                              --SPCQNGATCTDY-----LGGYSCKCVAGYHGVNCSEEIDECLS------
                                                                                                                                                                                                                      VAAQRQGVDVARLCQHGGLCVDAG-NTHHCRCQAGYTGSYCEDLVDECSP------
                                                                                                                                                                                                                                             IDPCADGVNGG--CHEHATCRMTGPGKHKCECKSHYVG----DGVD-CEPEQLPLDRCLQ 1041
                                                                                                                                                                                                                                                                                           PQGYTGP--NCQNLVHWC--DSSPCKNGGKCWQTHTQYRCECPSGWTGLYCDVPSVSC-E 1103
                                                                                                                                                                                                                                                                                                                             NLNYEGDGITC-TVVDFCKQNNGGCAKVAKCSQKGTQVSCSCKKGYKG-----DGYSCIE
                                                                                                                                                                                                                                                                                                                                                               CFNGGTCVDGI-NSFTCLCPPGFTGSYCQ---HVVNECDSRPCLLGGTCQDGRGLHRCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                           DCLPGFRGTFCEEDINECASDPCRNGANCTDCVDSYTCTCPAGFSGIHCENNTPDCTESS
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----CFNNGTCVDQVGGYSCTCPPGFVGE--RCEGDVNECL 1273
                                                                                                            QKAKYHLCSAGWLESGRVAYPTTYASQKCGANVVGI------VDYGSRANKSEM
                                                                                                                                                                                  DNGQCHPDASCADLYFQDTTVGVFHLRSPLGQYKLTFDKAKEACAKEAATIATYNQLSYA 1101
                                                                          ---HPCQNG---GTCLDLPNTYKC-SCPRGTQGVHCEINVDDCNPPVDPVSRSPK---
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RESULT 4 US-08-185-432-19 ; Sequence 19, Ap

Application US/08185432

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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212) 869-886
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2703 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Artavanis
APPLICANT: Busseau,
APPLICANT: Diederich
APPLICANT: Xu, Tian
APPLICANT: Matsuno,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCE ADDRESS:
CORRESPONDENCE ADDRESS:
PENNIE & EDMONDS
TO AVENUE Of the
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
 511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 18
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 21-JA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New York COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                             C-QSNPCL-NDGTCHDKINGFKCSCALGFTGARCQINIDDCQSQPCRNRGICHDSIAGYS
                                                                                                                                                                                                 KCAAGFRGNGTVC-TAINACETSNGGCSTKADCKRTTPGNRVCVCKAGYTG-----DGIV 374
                                                                                                                                                                                                                                                                                                                                                                                       KDWDQQGLMSQVLRYHVVGCQQLLLDNLKVTTSATTLQGEPVSISVSQDTVFINNEAKVL 570
                                                                                                         CECPPGYTGTS--CEININDCDSNPCHRGKC----IDDVNSFKCLCDPGYT--GYIC
                                                                                                                                        --CLPKYTGDGKVCSL-INVCLTN---NGGCSPFAFCNYTEQDQRICTCKPDYTGDGIVC 459
                                                                                                                                                                                                                                                NCSQGF--TGPRCETNINECESH--PCQNEGSC-LDDPGTFRCVCMPGFTGTQCEIDIDE 529
                                                                                                                                                                                                                                                                                                                   CHADAICDTSPINGSYACSCATGYKGVDCSEDI--DECDQGSPCEHNGICVNTP-GSYRC
                                                                                                                                                                                                                                                                                                                                                    C-VHGRCSQGPL-GDGSCDCDVGWRGVKCDMEITTDNCN--GTCHTSANCLLDPDGKASC 320
                                  QKQI-NECESNPCQFDGHCQDRVGSYYCQCQ-----AG-----TSGKNCEVNV
                                                                     RGSIYGELPKNP-----STSQYFFQLQEHAVRELAGPGPFTVFAPLSSSFNHEPRI 510
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Busseau, Isabelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : (212) 790-9090
(212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diederich, Robert J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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)N: 520
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DELTEX PROTEINS, NUCLEIC ACIDS, AND
ANTIBODIES, AND RELATED METHODS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/185,432
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US-08-185-432-17
                                                                                                                                                                                                                                        Patent No. 5750652 GENERAL INFORMATION:
                                                                                                                                                                                                                                                               Sequence 17, Application US/08185432 Patent No. 5750652
                                                                                                        APPLICANT: Matsuno, Kenji
TITLE OF INVENTION: DELTE:
TITLE OF INVENTION: ANTIB
                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                       1283 CVCQPGFV--GARCEGDINECL 1302
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                                                                                              NUMBER OF SEQUENCES:
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                      STREET:
CITY: N
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     STATE:
                                     ADDRESSEE: PENNIE & EDMONDS STREET: 1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                                           CQNGGTCHDRV----MNFSCSCPPGTMGII---CEINKDDCKPGACHNNGSCIDRVGGFE 1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSAGWLESGRVAYPTTYASQKCGANVVGIVDYGSRANKSEMWDVFCY-----RMKDVN 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITCT-VVDFCKQNNGGCAKVAKCSQKGTQVSCSCKKGYKGDGYSC-IEIDPCADGV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGINGY-NCSCLAGYSGANCQYK---LNKCDSNPCLNGATCHEQNNEYTCHCPSGFTGK- 1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGITGSGECLCETGWTAASCDTPTAVFAVC-TPACSVHATCTENN---TCVCNLNYEGDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIDCLLMNPTLGGRCDTFTTFDIPGEC---GSCI-----FTPK-CPLKSKPK 782
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                        New York
     New York
                                                                                                                                                                                   Diederich, Robert J.
                                                                                                                                                                                                      Busseau,
                                                                                                                                                                    Xu, Tian
                                                                                                                                                                                                                     Artavanis-Tsakonas, Spyridon
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                                                                                                             DELTEX PROTEINS, NUCLEIC ACIDS, ANTIBODIES, AND RELATED METHODS
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                                                                                                               COMPOSITIONS
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; TOPOLOGY: ur
; MOLECULE TYPE:
US-08-185-432-17
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Best Local :
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ZIP: 10036-Z/11
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: OVETEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 2556 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Sim thes 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212) - TELEFAX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
ALPPEQQDFLFNQDNKDKLKSYLKFHVIRDSKALASDLPRSASWKTLQGSELSVRC----
                                                                                                                                                                                                           LLLDNLKYTTSATTLQGEPVSISVSQDTVFINNEAKVLSSDIISTNGVIHVIDKLLSPKN 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QIGEFQCMCMPGYEG---VHCEVNTDECASSPCLHNGRCLDKIN-----EFQCECPTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKVLEIQKNRCDNNDTIIVRGEC--GKCSQQAPCPLE----TKPLRETR-----
                                                    ---TCEDGI-----NGFTCRCPEGY-----HDPTCLSEVNECNSNPCV------
                                                                                                     LLITPKDALGRVLQNLTTVAANHGYTKFSKLIQDSGLLSVITDSIHTPVTVFWPTDKALE
                                                                                                                                                            SPCDS - - - GTCLDKIDGYECACEPGYTGSMCNSNIDECAGNPCHNGG
                                                                                                                                                                                                                                                                    NAYLCF - - - - CLKGTTGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTGH--LCQYDVDECAST--PCKNGAKCLD-GPNTYTCVCTEGYTG-----THCEVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CPHGRTGLLCHLNDACISNPCNEGSNCDTNPVNGKAICTCPSGYTGPACSQDVDECSLG-
                                                                                                                                                                                                                                                                                                                   TSQYFFQLQEHAVRELAGPGPFTVFAPLSSSFNHEPRIKDWDQQGLMSQVLRYHVVGCQQ 532
                                                                                                                                                                                                                                                                                                                                                                       IDECDPDP-CHYGSCKDGVATFTCLCRPGYTGHHCETNINECSSQPCR--LWGTC-QDPD 622
                                                                                                                                                                                                                                                                                                                                                                                                                        NGGCSPFAFCNYTEQDQRI----CTCKPDYTG-----DGIVCRGSIYGELPKNPS 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDGKASCKCAAGFRGNGTVCTAINA--CETS----NGGCSTKADCKRTTPGNRVCVCKAG 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YGIHCDQACSCVHGRCSQGPLGDGSCDCDVGWRGVKCDMEITTDNC-NGTCHTSANCLLD 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -PAPGEVKMCALGTASV------WDGVNGTGTCQCGLGFNGTAC----ETCTEGK 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTCHNTHGGYNCVCVNGWTGE-----DCSENIDDCASAACFHGATCHDRVASFYCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YTGDGIVC-LEINPCLENHGGCDRNAECTQTGPNQAVCNCLPKYTGDGKVCSLINVCLTN 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -ANPCEHAGKCIN-----TLGSFECQCLQGYTGPRC--EIDVNECVSNPCQNDATC-LD
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20.6%;
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Pred. No. 1.3e-29;
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US-08-185-432-16
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                                                                                                                                                                                                                                                                                                                                                    Sequence 16, Application US/08185432 Patent No. 5750652
                                                                                                                                                                                                                                                                                                                                      GENERAL
ZIP: 1003b-2/1-
ZIP: 1003b-2/1-
ZIP: 1003b-2/1-
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: FLOOMPAtible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
There #1.0
                                                                                                                                                                                                                   APPLICANT: Xu, Tian
APPLICANT: Matsuno, Kenji
TITLE OF INVENTION: DELTE
TITLE OF INVENTION: ANTIB
                                                                                                                                                                                                                                                                            APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Busseau, Isabelle
APPLICANT: Diederich, Robert J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1263 E--RCEGDVNECL 1273
                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                STREET: 1155 AVE
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
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                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGQYKLTFDKAKEACAKEAATIATYNQLSYAQKAKYHLCSAGWLESGRVAYPTTYASQKC 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CECKSHYVG-----DGVD-CEPEQLPLDRCLQDNGQCHPDASCADLYFQDTTVGVFHLRSP 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DGFSCSGNLLQVL 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SC-----PWGTQGVHCEINVDDCNPPVDPVSWSPKCFNNGTCVDQVGGYSCTCPPGFVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---HVVNECDSRPCLLGGTCQDGRGLHRCTCPQGYTGP--NCQNLVHWC--DSSPCKNGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCETDIDDCWPNPCHNGGSCTDGINTAF - - CDCLPGFWGTFCEEDINECASDPCRNGANC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTCIDDVAGYKCNCLL--PYTGATCEVVLAPCAPSPCRNGGECRQSEDYESFSCVCP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KCWQTHTQYRCECPSGWTGLYCDVPSVSC-EVAAQRQGVDVARLCQHGGLCVDAG-NTHH 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KCSQKGTQVSCSCKKGYKG-----DGYSCIEIDPCADGVNGG--CHEHATCRMTGPGKHK 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPTAVFAVC-TPACSVHATCTEN----NTCVCNLNYEGDGITC-TVVDFCKQNNGGCAKVA 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -TAGAKGQTCEVDINECVLSPC---WHGASCQN-----THGXYRCHCQAGYSGR 903
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                                                                                                                                                                                                                                                                                                                                    INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -GTGSDIGELFLNEQMC-----RFIHR
                                                                                                                                                  E: PENNIE & EDMONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -LCWHGRFG-----PDCQPRSCSEHGQCDEGITGSGECLCETGWTAASCD 907
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                                                                                                                                                                                                DELTEX PROTEINS,
ANTIBODIES, AND R.
23
                                                                                                                                                   Americas
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 Version
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; MOLECULE TYPE: US-08-185-432-16
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Best Local Similarity
Matches 270; Conserv
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 2471 amino aci
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TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US,
FILING DATE: 21-JAN-19
CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 GVNGTGTCQCGLGFNGTACET------
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                                           TLQGSELSVRCGTGSDIGELF----LNEQMCRFIHRGLLFDVGVAYGIDCLLMNPTLGGR 753
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                                                                                                                                       HTPVTVFWPTDKALEALPPEQQDFLFNQDNKDKLKSYLKFHVIRDSKALASDLPRSASWK 697
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Pred. No. 6.9e-28;
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                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                               REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 73
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212,790-9090
                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: Misrock, S. Leslie
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                                                                SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release "."
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COMPUTER: IF
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החסשפת: 1155 Avenue
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TELEX: 66141 PENNIE
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                STRANDEDNESS:
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                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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TOPOLOGY:
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GCAKVAKCSQKGTQVSCSCKKGYKGDGYSC-IEIDPCADGVNGGCHEHATCRMTGPGKHK 1015
                                                                    WTAASCDTPTAVFAVCTPACSVHATCTEN---NTCVCNLNYEGDGITC-TVVDFCKQNNG
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Pred. No. 6.9e-28;
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REFERENCE/DOCKET NUMBER: 7326
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-909
TELEFAX: 212 8698864/9741
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
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Patent No. 6083904
GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, S
                                                                                                                                          Best Local Similarity Matches 270; Conserv
                                                                                                                                                             Query Match
Best Local S
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PRIOR APPLICATION DATA:
APPLICATION UMBER: 08/083
FILING DATE: 25-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Therapeutic And Diagnostic
TITLE OF INVENTION: And Compositions Based on N
TITLE OF INVENTION: Nucleic Acids
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                  169 RKCIYSIYFMGKRSVFIGCQPQCVRTIITRACWLASLAHNAKPAPGEVKMCALGTASVWD 228
                                                                                                   133 QKNRCDNNDTIIVRGECGKC------SQQAPCPLETKPL-----RET 168
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                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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No. 6083904ch Proteins And
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968		843	QY Db	
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956)1 WTAASCDTPTAVFAVCTPACSVHATCTENNTCVCNLNYEGDGITC-TVVDFCKQNNG	901	VQ	
786	CIHGNCTGGLSGYKC-LCDAGWVGINCEVDKNECL		Db	
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606	88 HTPVTVFWPTDKALEALPPEQQDELFNQDNKOKLKSYLKFHVIRDSKALASDLPRSASWK 	580	da Qy	
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637	44 -IDKLLSPKNILLITPKDALGRVLQNLTTVAANHGYTKFSKLIQDSGLLSVITDSI		Qy	
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537	3 -PCHKGALCDINPLNGQYICTCPQGYXGADCTEDVDECAMANSNPC	383 480	סַּלַ	
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276	! LYVPCAPSPCVNGGTCROTGDFTFECNCLPGFEGSTCERNIDDCPNHRCQNGGVCV		Db	
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; Sequence 2, Application
; Patent No. 5869282
; GENERAL INFORMATION:
                   Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-400-159-2
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 274; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Fleming, R
APPLICANT: Artavanis
APPLICANT: Mann, Robe
APPLICANT: Gray, Grac
TITLE OF INVENTION: N
TITLE OF INVENTION: N
TITLE OF INVENTION: S
TITLE OF SEQUENCES:
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APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/400,159
FILING DATE: 07-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistorck, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 73:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                     403
                                                         397
                                                                                                                              341
                                                                                                                                                                                               296 DR----PGECECRPGWRGPLCNECMYYPGCKHGSCNGSA-----WKCVCDTNWG 340
                                                                                                                                                                                                                        237 QCGLGFNGTACET-----CSCVHGRC 270
                                                                                          389 DRNAECTQTGPNQA-----
                                                                                                                                                               330 GTVCTA-INACETSNGGCSTKADCKRTTPGNRVCVCKAGYTGDGIVCLEINPCLENHGGC 388
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STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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                                                   RNGGTCTLKTSNRTQAQVYRTSHGRSNMGRPVRRSSSMRSLDHLRPEGQALNGSSSSGLV 456
                                                                                                                          GILCDQDLNFCGT-HEPCKHGGTCENTAPDKYRCTCAEGLSGEQCEIVE-HPCATR--PC
                 -----VCNCLPKYTGDGKVCSLINVCLTNNGGCSPFAFCNYTEQDQRICT 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RY: USA
10036-2711
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Henrique, Domingos M.P.
Lewis, Julian H.
                                                                                                                                                                                                                                                                                                                                               5.3%; Score 413.5; DB 2; Length 1404; ilarity 19.7%; Pred. No. 3.4e-25; Conservative 127; Mismatches 482; Indels 507;
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Gray, Grace E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Artavanis-Tsakonas, Spyridon
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                                                                                                                          396
                                                                                          402
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1319	EFFEKSNNI,ONFENI,RRYTNDI.KGSTSGI.RAATGMEI.GLUDADFI.AASAASSSAI.	1266	Dh
1405	RRHPQSPPVTPSQTLENRI	1355	Qy
1265	ETARVADGSGHS-LLIGVLCGVFIVLVGFSVFISLYWKQRLAYRTSSGMNLTPSLDALRH	1207	Db
1354	RAPPTAATAHSGLGTGIFCAVVLVTGAIALAAYSYFRLKQRTT	1311	Qy
1206	: RRKELELQHAKLAALTSIVEVKL	1147	Db
1310		1268	Qy
1146	CARLTILLALERVGKGASVEGLCSLVRVLLAAQLIKKPASTFGQDPGMLMVLCDLKTGTN	1087	dd
1267		1237	Оу
1086	VNEN	1029	Db
1236	QVLMSEPSLTNFLTEVLAFSKSSARGQAFLKHLTDLSIRGTLFVPQNSGLPGNKSL	1181	Qy
1028	TEDDENCNACVCENGTSRCTNLWCGLPNCYKVDPLSKSSNLS	987	Db
1180	VFCYRMKDVNCTCKAGYVGDGFSCSGNLL	1121	Qy
986	ALTGR	938	Db
1120	AKYHLCSAGWLESGRVA	1068	Qy
937		892	Db
1067	GDGVDCEPEQLPLDRCLQDNGQCHPDASCADLYFQDTTVGVFHL	1008	Qy
891	QNGGTCMPGAPDKALQPHCRCAPGWTGLFCAEAIDQCRGQPCHNGGTCE	843	Db
1007	GVNGGCHEHATCR	949	Qy
842	-DGDFTCECMSGWTGKRCSERATGCYAGQC	814	DЬ
948		889	Qy
813	LPCSGHGSCEMSDVGTFCKCHVGHTGTFCEHNLNECSPNPCRNGGICLDG	764	Db
888		831	Qy
763	EQLRPLCSQPPCNEGCFANVSLATSATTTTTTTTTTTTTKMAKPSG	717	Db
830	/IQTPRCCHGYFMPDCQACPGG	791	Qy
716	VGKFNCICPLGYSGSLCEEAKENCTPSPCLEGHCLNTPEGYYCHCPPDRAGKHC	663	Db
790	YΙ	738	Оу
662		639	Db
737	LSVRCGTGSDIGELFLNEQMCRFIHRGLLFDVGV	678	Qy
638		625	Db
677	IQDSGLLSVITDSIHTPVTVFWPTDKALEALPPEQQDFLFNQDNKDKLKSYLKF	624	Qy
624	Ļ-	566	Db
623	FSKL	568	Qy
565		533	Db
567	VSQDTVFINNEA	508	Оу
532	CPPEWHGDVCQVDVNECEAPVNECEAP	513	Db
507	YGELPKNPSTSQYFFQLQEHAVRELAGPGPFTVFAPLSSSFNHE	448	Qy
512	SLGSLQLQQQLAPDFTCDCAAGWTGPTCE-INIDECAGGPCEHGGTCIDLIGGFR-CE	457	Db

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                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: unknown ; MOLECULE TYPE: protein US-08-611-729A-2
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US-08-611-729A-2
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,729A
FILING DATE: 06-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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APPLICANT:
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TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1404 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                      236
389 DRNAECTOTGPNQA--
                                          341
                                                                            330 GTVCTA-INACETSNGGCSTKADCKRTTPGNRVCVCKAGYTGDGIVCLEINPCLENHGGC
                                                                                                                          296
                                                                                                                                             271 SQGPLGDGSCDCDVGWRGVKCDMEITTDNC-NGTCHTSANCLLDPDGKASCKCAAGFRGN 329 : | |:| || || : | :|:|:|| || ||
                                                                                                                                                                                                                                        237 QCGLGFNGTACET------CTEGKYGIHCDQA-----CSCVHGRC 270
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CITY: N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Pennie & Edmonds STREET: 1155 Avenue of the Americas
                                          GILCDQDLNFCGT-HEPCKHGGTCENTAPDKYRCTCAEGLSGEQCEIVE-HPCATR--PC 396
                                                                                                                        DR----PGECECRPGWRGPLCNECMVYPGCKHGSCNGSA-----
                                                                                                                                                                                                      QCAVTYYNTTCTTFCRPRDDQFGHYACGSEGQKLCLNGWQGVNCEEAICKAGCDPVHGKC 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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Henrique, Domingos M.P.
Lewis, Julian H.
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Artavanis-Tsakonas, Spyridon
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                                                                                                                        ---WKCVCDTNWG
                                                                                                                        340
    402
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Db	397	RNGGTCTLKTSNRTQAQVYRTSHGRSNMGRPVRRSSSMRSLDHLRPEGQALNGSSSSGLV 456	
Qy	403		
Db	457	SLGSLQLQQQLAPDFTCDCAAGWTGPTCE-INIDECAGGPCEHGGTCIDLIGGFR-CE 512	
Qy	448	CKPDYTGDGIVCRGSIYGELPKNPSTSQYFFQLQEHAVRELAGPGPFTVFAPLSSSFNHE 507	
DЬ	513	CPPEWHGD-VCQVD	
Qy	508	PRIKDWDQQGLMSQVLRYHVVGCQQLLLDNLKVTTSATTLQGEPVSISVSQDTVFINNEA 567	
DЬ	533		
Qy	568	KVLSSDIISTNGVIHVIDKLLSPKNLLITPKDALGRVLQNLTTVAANHGYTKFSKL 623	
рb	566	SAVASTSLAIGPCINAKECRNQPGSFACICKEGWGGVTCAENLDDCVGQCRNGATCID-L 624	
Qy	624	IQDSGLLSVITDSIHTPVTVFWPTDKALEALPPEQQDFLFNQDNKDKLKSYLKF 677	
Db	625	VNDYRCACASGETG	
Qy	678	HVIRDSKALASDLPRSASWKTLQGSELSVRCGTGSDIGELFLNEQMCRFIHRGLLFDVGV 737	
Db	639	RDCETDIDECATSPCRNGGEVDM 662	
Qy	738	AYGIDCLEMNPTLGGRCDTFTTFDIPGECGSCIFTPKCPLKSKPKGVKKKCIY 790	
рь	663	VGKFNCICPLGYSGSLCEEAKENCTPSPCLEGHCLNTPEGYYCHCPPDRAGKHC 716	
Qy	791	1	
Db	717	EQLRPLCSQPPCNEGCFANVSLATSATTTTTTTTTTTTTTTKMAKPSG 763	
Qy	831	PDTPCNNRGMCRDLYTPMGQCLCHTGFNGTACELCWHGRFGPDCQPRSCSEHGQCDEG 888	
Db	764	LPCSGHGSCEMSDVGTFCKCHVGHTGTFCEHNLNECSPNPCRNGGICLDG 813	
Qy	889	SCDTPTAVFAVCT	
Db	814	-DGDFTCECMSGWTG	
Qy	949	DFCKQNNGGCAKVAKCSQKGTQVSCSCKKGYKGDGYSCIE-IDPCADGVNGGCHEHATCR 1007	
Db	843	QNGGTCMPGAPDKALQPHCRCAPGWTGLFCAEAIDQCRGQPCHNGGTCE 891	
Qy	1008	VGDGVDCEPEQLPLDRCLQDNGQCHPDASC	
Db	892	-SGAGWERCVCAQGE SGPDC RINVNECSPQ PCQGGATCID GIGGYSC 937	
Qy	1068	RSPLGQYKLTFDKAKEACAKEAATIATYNQLSYAQKAKYHLCSAGWLESGRVA 1120	
Db	938	ĀΙ	
Qy	1121	VVGIVDYGSRANKSEMWDVFCYRMKDVN ; ; ;	
Db	987	TEDDENCNACVCENGTSRCTNLWCGLPNCYKVDPLSKSSNLS 1028	
Qy	1181	QVLMSFPSLTNFLTEVLAFSKSSARGQAFLKHLTDLSIRGTLFVPQNSGLPGNKSL 1236	
Db	1029	GVCKOHEVCVPALSETCLSSPCNVRGDCRALEPSRRVAPPRLPAKSSCWPNQAVVNEN 1086	
Qy	1237		
Db	1087	CARLTILLALERVGKGASVEGLCSLVRVLLAAQLIKKPASTEGQDPGMLMVLCDLKTGTN 1146	
Оу	1268	SQDQLHQ	
Db	1147	DTVELTVSSSKLNDPQLPVAVGLLGELLSSRQLNGIQRRKELELQHAKLAALTSIVEVKL 1206	
Qy	1311	-VLVTGAIALAAYSYFRLKQRTT 135	
Db	1207	77)	

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                                                                                                                                                                             Query Match
Best Local Similarity
Matches 231; Conserv
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                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (212) 869-97
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION UNMEER: US/08/400,159
FILING DATE: 07-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1193 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 73
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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309 NCLLDPDGKASCKCAAGERGNGTVC-TAINACETS---NGGCSTKADCKRTTPGNRVCVC
                                                 238 KCIPHP-----GCVHGTC----IEPWQCLCETNWGGQLCDKDLNYCGTHPPCLNGG
                                                                                                                     201
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STATE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Pennie & Edmonds STREET: 1155 Avenue of the Americas
                                                                                                                                                POCVRTIITRACWLASLAHNAKPAPGEVKMCALGTASVWDGVNGTGTCOCGLGFNGTACE
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                                                                                   TCTEGKYGIHCDQACSCVHGRCSQGPLGDGSCDCDVGWRGVKCDMEITTDNCNGTCHTSA
                                                                                                                 New York
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                                                                                                                                                                                                                                                                                                              amino acid
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(212) 869-9741/8864
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                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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Myat, Anna M.
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                                                                                                                                                                              5.2%; Score 410; DB 2; I
22.0%; Pred. No. 5.1e-25;
ative 72; Mismatches 323;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE AND PROTEIN SEQUENCES OF
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RESULT 12
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                                                                                                    DKAKEACAKEAATIATYNQLSYAQKAKYHLCS 1110
                                                                                                                                     VP--VKEDHCFTHPCAAVGECWPSNQQPVKTKCNSDSYYQDNCANI--
                                                                                                                                                                                                        GRPCFTSIRVMPDGAKWDDDCNTCQCLN-GKVTCSKVWCGPRPCIIHAKGHNECPAGHAC
                                                                                                                                                                                                                                                                          YRCECAPGFAGPDCRININECQSSPCAFGATCVDEINGYRCI----CPPGRSGPGCQEVT
                                                                                                                                                                                                                                                                                                            --CSCKKGYKG-----
                                                                                                                                                                                                                                                                                                                                              CHNGGTCVVSGDSFTCVCKEGWEGP--TCT----QNTNDCSP-HPCYNSGTCVDGDNW
                                                                                                                                                                                                                                                                                                                                                                               CSVHATCT - - - ENNTCYCNLNYEGDGITCTVVDFCKQNNGGCAKVAKCSQKGTQVS - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                 C----HSR-DSQCDEATCNNGGTCYDEGDT--FKCMCPAGWEGATCN--IARNSSCLPNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CELCWHGRFGPDCQPRSCSEHGQC-DEGITGSGECLCETGWTAASCDTPTAVFAVCTP-A 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTVVIQTPRCCHGYFMPDCQA----CPGGPDTPCNNRGMCRDLYTPMGQCLCHTGFNGTA
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                                                                                                                                                                       EPEQLPLDRCLQDN----
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                                                                                                                                                                      -GQCHPD-----ASC-ADLYFQDTTVGVFHLRSPLGQYKLTF 1078
                                                                                                                                                                                                                                        TCRMTGPGKHKCE-----CKSHYVGD-----GVDC
                                                                   ---EHICS
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Sequence 10, Application US/08611729A Patent No. 6004924

GENERAL INFORMATION: APPLICANT: Ish-Ho

APPLICANT:
APPLICANT:
APPLICANT:

Lewis, Julian H. Myat, Anna M. Fleming, Robert Henrique, Ish-Horowicz,

Domingos

X . □

Anna M. ng, Robert J

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212) 869-9741/88
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-037
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9990
TELEPAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION: NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Mann, Robert S.
APPLICANT: Gray, Grace E.
567 AKVLSSDIISTNGVIHVIDKLLSPKNLLITPKDALGRVLQNLTTVAANHGYTKFSKLIQD 626
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CITY: New York
STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid TOPOLOGY: unknown
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ZIP: 10036-2711
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                                                                                                                                                                                                                                       ECEGKPCVNANSCRNLIGSYYCDCITGWSGHNCDININDCRGQCQNGGSCRDLVNGYR-C 447
                                                                                                                                                                                                                                                                               --DGKVCSLINV-------CLTN------NGGCSPFAFCNYTEQDQRIC 446
                                                                                                                                                                                                                                                                                                                         APGWAGPTCTDNIDDCSPNPC--GHGG-----TCQDLVDGFKCICPPQWTGKTCQLDAN 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTEGKYGIHCDQACSCVHGRCSQGPLGDGSCDCDVGWRGVKCDMEITTDNCNGTCHTSA 308
                                                                                                       EPRIKDWDQQGLMSQVLRYHVVGCQQLLLDNLKYTTSATTLQGEPVSISVSQDTVFINNE 566
                                                                                                                                                                                           TCKPDYTGDGIVCRGSIYGELPKNPSTSQYFFQLQEHAVRELAGPGPFTVFAPLSSSFNH 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KCIPHP-----GCVHGTC----IEPWQCLCETNWGGQLCDKDLNYCGTHPPCLNGG 284
                                                                                                                                                   ICSPGYAGDH---CEKDI-NECASNPCMN------GGHCQDEING---FQCLCPAGFSGN- 494
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                                                               NUCLEOTIDE AND PROTEIN SEQUENCES OF THE SERRATE GENE AND METHODS BASED THEREON
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	NAME: Campbell, Cathryn A.	2	
	CLASSIFICATIO	A H	
	CATION NUMBER	(
	PC-DOS In Relea DATA	3	
	IBM PC compatible		
	PUTER READABL	co	
	COUNTRY: USA ZIP: 92122		
	Ca		·· ··
	TREET: 4370 La Jolla Village		
	RRESPONDENCE ADDRESS: ADDRESSEE: Campbell & F	00	
	R OF SEQUENCES: 110	N.	
	INVENTION:	7 17 17 17 17 17 17 17 17 17 17 17 17 17	
	, Nancy B.	AP	.
	ANT: Hood, Leroy	AP	
	INF	GENERAL	
		Sequence Patent No	
)46-7	SULT:	(O H
		ų.	Дb
	79 DKAKEACAKEAATIATYNQLSYAQKAKYHLCS 1110	107	Qy
TF 938	93 VPVKEDHCETHPCAAVGECWPSNQQPVKTKCNSDSYYQDNCANI	80	Db
QYKLTF 1078	.030 EPEQLELDRCLQDNGQCHPDASC-ADLYFQDTTVGVFHLRSPLGQYKLTF	10	Qy
PAGHAC 892	34 GRPCFTSIRVMPDGAKWDDDCNTCQCLN-GKVTCSKVWCGPRPCIIHAKGHNECPAGHAC	00	Db
GVDC 1029	.005CKSHYVGD	10	Qy
GCQEVT 833	8 YRCECAPGFAGPDCRININECQSSPCAFGATCVDEI	77	DЬ
ССНЕНА 100-	973CSCKKGYKG	9	Qγ
.VDGDNW 777	27 CHNGGTCVVSGDSFTCVCKEGWEGPTCTQNTNDCSP-HPCYNSGTCVDGDNW	7	Дd
VS 972	NNTCVCNLNYEGDGITCTV	9	Qy
IARNSSCLPNP 726	HSR-DSQCDEATCNNGGTCYDEGDTFKCMCPAGWEGATCN	6	DЬ
VCTP-A 919	G	80	Qу
FCECKNGWKGKT 675	LVNDF-	6	Дb
GFNGTA 861	INRGMCRDLYTPMGQC	80	Qy
628	10 NPCKNGGTCIDGVNSYKCI	6	Дb
RRNVEGCONL 805	CIFTPKCPLKSKPKGVKK-KCIYNPLPF	7	Qy
NDC-ES 609	76HGKCKSQAGGKFTCECNKG····-FTGTYCHENI	57	da
IDCLLM 746	87 ASDLPRSASWKTLQGSELSVRCGTGSDIGELFLNEQMCRFIHRGLLFDVGVAYG	6	Qy
GP 575	51 SCTVAVASNSTPEGV	ر. د	Db
IRDSKAL 686	VITDSIHTPVTVEWPTDKALEALPPEQQDFLFNQDNKDKLKSYLKFHV	6	Оу
CEVI-D 550	25KDHCRTTPCEVI	ر. د	DЬ

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: P-UW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS: LENGTH: 1010 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
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KCMCPGGWEGTTCN--IARNSSCLPNPCHNGGTCVVNGESFTCVCKEGWEG------P
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                          ECLCETGWTAASCDTPTAVFAVCTP-ACSVHATCTENN---TCVCNLNYEGDGITCTVVD
                                                           CHNGGTCRDLVNDF-YCDCKNGWKGKTC----HSR-DSQCDEATCNNGGTCYDEG--DAF
                                                                                          CNNRGMCRDLYTPMGQCLCHTGFNGTACELCWHGREGPDCQPRSCSEHGQC-DEGITGSG
                                                                                                                           --DGVNSYKCI---
                                                                                                                                                     KPKGVKK-KCIYNPLPFRRNVEGCQNLCTVVIQTPRCCHGYFMPDCQA----CPGGPDTP
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Pred. No. 2.9e-24;
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LENGTH: 1036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SAKANO, APPLICANT: ITOH, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE FILE REFERENCE: KP-8447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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                                                                             ICTCKPDYTGDGIVCRGSIYGELPKNPSTSQYFFQLQEHAVRELAGPGPFTVFAPLSSSF
                                                                                                                     -----NAKSCKNLIASYYCDCLPGWMGQN--CDININDCL---GQCQNDASCRDLVNGYR 441
                                                                                                                                                        GGCDRNAECTQTGPNQAVCNCLPKYTGDGKVCSL-INVCLTNNGGCSPFAFCNYTEQDQR
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-RIKDW-----DQQGLMSQVLRYHVVGCQQLLLDNLK 539
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FCKCPEDYEGKNCSHLKDHCR	RESULT 15 US-09-068-740A-7 IS Sequence 7, Application US/0906 PATENT NO. 6337387 GENERAL INFORMATION: APPLICANT: SAKANO, SEIJI APPLICANT: ITOH, AKIRA TITLE OF INVENTION: 'DIFFERENT FILE REFERENCE: KP-8447 CURRENT APPLICATION NUMBER: US CURRENT FILING DATE: 1998-06- PRIOR APPLICATION NUMBER: JP PRIOR APPLICATION NUMBER: JP PRIOR APPLICATION NUMBER: JP PRIOR FILING DATE: 1995-11-17 PRIOR APPLICATION NUMBER: PCT PRIOR FILING DATE: 1996-11-15 NUMBER OF SEQ ID NOS: 48 SOFTWARE: PATENTIN NOS: 48 ORGANISM: Homo Sapiens US-09-068-740A-7	QY 1083 EACAKEAATIA-TYN-QLSYAQ ;; ;; ; Db 915 TKCTSDSYYQDNCANITFTENKEMMSPG	Qy 1039CLQDNGQCHPDASC.	Qy 994DGVNG-GCHEHATCR-MTG	Qy 950 FCKQNNGGCAKVAKCSQKGTQVS- 	Qy 894 ECLCETGWTAASCDTPTAVFA : : : : : : Db 697 KCMCPGGWEGTTCNIARNS	Qy 835 CNNRGMCRDLYTPMGQCLCHTGENG	Qy 780 KPKGVKK-KCIYNPLPERRNV	Qy 720 NEQMCRETHRGLLEDVGVAYG : : Db 592 GTYCHENI	Qy 660 DFLFNQDNKDKLKSYLKFHVI Db 573	Db 571HG	QY 600 ALGRVLQNLTTVAANHGYTKFS	Qy 540 VTTSATTLOGEPVSISVSQDTVF	Db 489 NLCQLDIDYCEPNPCQNGAQCYNRASDY
	8740A IATION-SUPPRESSIVE /09/068,740A 18 7-299611 7-311811 /JP96/03356	KAKYHLCS : LTTEHICS	ADLYFQDTTVGVFHLRSPLGQYKLT	PGKHKCECKSHYVGDGVDCEPEQLPLDR	CSCKKGYKGDGYSCIEIDPCA	P-ACSVHATCTENNTCVCNLNYEGDGITCTVVD	TACELCWHGRFGPDCQPRSCSEHGQC-DEGITGSG	EGCQNLCTVVIQTPRCCHGYFMPDCQACPGGPDTP	IDCLLMNPTLGGRCDTFTTFDIPGECGSCIFTPKCPLKS	RDSKALASDLPRSASWKTLQGSELSVRCGTGSDIGELFL	1	KLIQDSGLLSVITDSIHTPVTVFWPTDKALEALPPEQQ	VFINNEAKVLSSDIISTNGVIHVIDKLLSPKNLLITPKD ::	FCKCPEDYEGKNCSHLKDHCR

Db 861 CSKVWCGPRPCLLHKG	Qy 1039	Db 804 CVDEINGYRO	Oy 994 DGVNG-GC	Db 747 ICAQUINDCS	Qy 950 FCKQNNGGC	Db 697 KCMCPGGWEGTTCN-	Qy 894 ECLCETGWT	Db 645 CHNGGTCRDLVNDF	QY 835 CNNRGMCRDI	Db 615 DGVNSYKC	Qy 780 KPKGVKK-KC	Db 592 GTYCHENI	Qy 720 NEQMCRFIHRG	Db 573	QY 660 DFLFNQDNKDKLKS	Db 571	Qy 600 ALGRVLQNLT	Db 538 -TTPCEVIDSCTVAMA-	Oy 540 VTTSATTLOG	Db 489 NLCQLDIDYC	Qy 505 NE	Db 442 -CICPPGYAGDH-	Qy 445 ICTCKPDYTC	Db 392NAKSC	Qy 386 GGCDRNAECT	Db 339 TCSTNIDDCS	Qy 331 TVCTAINACE	Db 280 TCSNTGPDKYQC	Qy 303 TCHTSA	Db 233 KCIPHP	Qy 249 ТСТЕСКҮСІН	Db 196 PECNRAICROGC	Qy 189 PQCVRTIITE
PCLLHKGHSECPSGQSCIPILDDQCFVHPCTGVGEC	-CLQDNG9CHPDASCADLYFQDTTVGVFHLRS	CVDEINGYRCVCPPGHSGAKCQEVSGRPCITMGSVIPDGA	CHEHATCR-MTGPGKHKCECKSHYVGDGV	F-HPCYNSGTCVDGDNWYRCECAPGFAGP-	FCKQNNGGCAKVAKCSQKGTQVSCSCKKGYKGDGYSC	TTCNIARNSSCLPNPCHNGGTCVVNGESFTCVCKEGWEG	PTAVFAVCTP-ACSVHATCTENN	YCDCKNGWKGKTCHSR-	GQCLCHTGFNGTACELCWHGRF		KCIYNPLPFRRNVEGCQNLCTVVIQTPRCCHGYFMPDC	ENTNDC-ESNPCRNG	LLFDVGVAYGIDCLLMNPTLGGRCDTFTTFD	KCKSQSGG)KLKSYLKFHVIRDSKALASDLPRSASWKTLQGSELSVRCGTGSD	HG	LGRVLQNLTTVAANHGYTKFSKLIQDSGLLSVITDSIHTPVT	SNDT	· 👸	NLCQLDIDYCEPNPCQNGAQCYNRASDYFCKCPEDYEGKNCSHLKDH-	HEPRIKDWDQQGLMSQVLRYHVVG	DHCERDI-DECASNPCLNGGHCQNEI-	GDGIVCRGSIYGELPKNPSTSQYFFQLQEHAVRE	NAKSCKNLIASYYCDCLPGWMGQNCDININDCL	QTGPNQAVCNCLPKYTGDGKVCSL-INVCLTNN	SPNNCSHGGTCQDLVNGFK-CVCPPQWTGKTCQLDANEC-	- 8	CSCPEGYSGPNCEIAEHACLSDPCHNRGSCKETS	NCLLDP-DGKAS		TCTEGKYGIHCDQACSCVHGRCSQGPLGDGSCDCDVGWRGVKCDME	SPKHGSCKL	WLASLAHNAKPAPGEVK
GECRSSSLQPVK 914	RSPLGQYKLTFDKAK 1	ITMGSVIPDGAKWDDDCNTCQCLNGRIA 860	VDCEPEQLPLDR 1038	-DCRININECQSSPCAFGAT 803	CIEIDPCA 993	CVCKEGWEGP 746	TCVCNLNYEGDGITCTVVD 949	DSQCDEATCNNGGTCYDEGDAF 696	RSCSEHGQC-DEGITGSG 893	CSDGWEGAYCETNINDCSQNP 644	MPDCQACPGGPDTP 834	GTCI 614	IPGECGSCIFTPKCPLKS 779	QSGGKFTCDCNKGFT 591	SELSVRCGTGSDIGELFL 719	572	IHTPVTVFWPTDKALEALPPEQQ 659	PEGVRYISSNVCGP 570	HVIDKLLSPKNLLITPKD 599	: : HLKDHCR 537	VLRYHVVGCQQLLLDNLK 539	EINRFQCLCPTGFSG 488	QYFFQLQEHAVRELAGPGPFTVFAPLSSSF 504	-GQCQNDASCRDLVNGYR 441	INVCLTNNGGCSPFAFCNYTEQDQR 444	CQLDANEC-EAKPCV 391	EINPC	ETSLGFECECSPGWTG-P 338	- 1	PWQCLCETNWGGQLCDKDLNYCGTHQPCLNGG 279	CDMEITTDNCNG 302	PGDCRCQYGWQGLYCD 232	NGTGTCQCGLGFNGTACE 248

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Minimum
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Perfect score:
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5175.5
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// Cgn2_6/ptodata/2/paa/US09_COMB.pep: *
// Cgn2_6/ptodata/2/paa/US09_COMB.pep: *
// Cgn2_6/ptodata/2/paa/US092_COMB.pep: *
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PCT-US01-13403-62

PCT-US01-13403-62

2 US-09-842-930A-25

6 US-60-230-445-1388

PCT-US01-13403-63
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               Sequence 2, Appli
Sequence 25, Appli
Sequence 25, Appl
Sequence 62, Appl
Sequence 25, Appl
Sequence 21388, Ap
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ALIGNMENTS

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APPLICANT: WEIGEL, PAUL H.
APPLICANT: WEIGEL, BIN
APPLICANT: WEIGEL, JANET A.
APPLICANT: WEIGEL, JANET A.
TITLE OF INVENTION: IDENTIFICATION AND USES OF
FILE REFERENCE: 618754/JP/199,538
CURRENT APPLICATION NUMBER: PCT/US01/13403
CURRENT FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 60/245,320
PRIOR APPLICATION NUMBER: 60/245,320
PRIOR APPLICATION NUMBER: 60/29,538
PRIOR APPLICATION NUMBER: 60/199,538
PRIOR APPLICATION NUMBER: 60/199,538
PRIOR FILING DATE: 2000-04-25
NUMBER DE SEO IT DANCE: 64
                                                                                                              PCT-US01-13403-2
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                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 1431
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    Matches 1431;
                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 64
                                                                                                                            TYPE: PRT
ORGANISM: Rattus norvegicus
    Conservative
                      100.0%;
  0;
                      Score 7861;
Pred. No. 0;
Mismatches
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                                           DB 1;
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  0;
                                           Length 1431;
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  0;
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           AKEACAKEAATIATYNQLSYAQKAKYHLCSAGWLESGRVAYPTTYASQKCGANVVGIVDY
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AKEACAKEAATIATYNQLSYAQKAKYHLCSAGWLESGRVAYPTTYASQKCGANVVGIVDY
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DЬ

Qy

Db Db Вþ

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APPLICANT: Weigel, Paul
APPLICANT: Weigel, Paul
FILE OF INVENTION: Identification of Hyaluronan Rec
FILE REFERENCE: 5820.603
CURRENT APPLICATION UNMBER: US/09/842,930A
CURRENT FILING DATE: 2001-04-22
PRIOR APPLICATION NUMBER: 60/245,320
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: 60/199,538
PRIOR FILING DATE: 2000-04-25
INUMBER OF SEQ ID NOS: 56
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 1431
TYPE: PRT
ORGANISM: Rattus norvegicus
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US-09-842-930A-2
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                                                                                GFNGTACETCTEGKYGIHCDQACSCYHGRCSQGPLGDGSCDCDVGWRGVKCDMEITTDNC
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                                                     HSGLGTGIFCAVVLVTGAIALAAYSYFRLKQRTTGFQRFDQKRTLMSWLLASSSPRISQT
                                                                                               FLRTMLGSQLLITFSQDQLHQETRFVDGRSILQWDIIAANGILHIISEPLRAPPTAATAA
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PCT-US01-13403-25; Sequence 25, Appl; GENERAL INFORMATI; APPLICANT: WEIGE
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PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: 60/199,538
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 25
LENGTH: 1394
TYPE: PRT
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Best Local Similarity
Matches 1063; Conser
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APPLICANT: ZHOU, BIN
APPLICANT: WEIGEL, JANET A.
TITLE OF INVENTION: IDENTIFICATION AND USES
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CURRENT APPLICATION NUMBER: PCT/US01/13403
CURRENT FILING DATE: 2001-04-25
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                                               NLTQDSGLLSVITDPIHTPVTLFWPTDQALHALPAEQQDFLFNQDNKDKLKEYLKFHVIR
                                                                           KLIQDSGLLSVITDSIHTPYTVFWPTDKALEALPPEQQDFLFNQDNKDKLKSYLKFHVIR
                                                                                                      YINNKAKIISSDIISTNGIVHIIDKLLSPKNLLITPKDNSGRILQNLTTLATNNGYIKFS
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: Sequence 62, Application PC/TUS0113403
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ORGANISM: Homo sapiens
PCT-US01-13403-62
                                                     SEQ
                                                                                                                                               APPLICANT: WEIGEL, JANET A.

TITLE OF INVENTION: IDENTIFICATION AND USES
FILE REFERENCE: 618754/JP/199,538

CURRENT APPLICATION NUMBER: PCT/US01/13403

CURRENT FILING DATE: 2001-04-25
                                                               PRIOR APPLICATION NUMBER: 60/245,320 PRIOR FILING DATE: 2000-11-02 PRIOR APPLICATION NUMBER: 60/199,538 PRIOR FILING DATE: 2000-04-25 NUMBER OF SEQ ID NOS: 64 SOFTWARE: Patentin Ver. 2.1
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                          TYPE: PRT
                                      Q ID NO 62
LENGTH: 1192
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NFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENETLSGRDIEHHLANVSM
        NFLTEVLAFSKSSARGQAFLKHLTDLSIRGTLFVPQNSGLPGNKSLSGRDIEHHLTNVNV 1250
                                  GSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNCTCKVGYVGDGFSCSGNLLQVLMSFPSLT
                                          GANVVGIVDYGSRANKSEMWDVFCYRMKDVNCTCKAGYVGDGFSCSGNLLQVLMSFPSLT
                                                                                                     PDAPCNNRGVCLDQYSATGECKCNTGFNGTACEMCWPGRFGPDCLPCGCSDHGQCDDGIT
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CURRENT APPLICATION NUMBER: US/09/842,930A
CURRENT FILING DATE: 2001-04-22
PRIOR APPLICATION NUMBER: 60/245,320
PRIOR FILING DATE: 2000-11-02
PRIOR FILING DATE: 2000-04-25
PRIOR RILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 56
SOFTMARE: Patentin version 3.1
SEQ ID NO 25
LENGTH: 1394
TYPE: PRT
ORGANISM: Homo sapiens
US-09-842-930A-25
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                                                       CNYTEQDQRICTCKPDYTGDGIVCRGSIYGELPKNPSTSQYFFQLQEHAVRELAGPGPFT
                                                                                                                          LEINPCLENHGGCDRNAECTOTGPNQAVCNCLPKYTGDGKVCSLINVCLTNNGGCSPFAF
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VFAPLSSSFNHEPRIKDWDQQGLMSQVLRYHVVGCQQLLLDNLKVTTSATTLQGEPVSIS
                                    CNHTGQVERTCTCKPNYIGDGFTCRGSIYQELPKNPKTSQYFFQLQEHFVKDLVGPGPFT
                                                                                                           LEINPCLENHGGCDKNAECTQTGPNQAACNCLPAYTGDGKVCTLINVCLTKNGGCSEFAI 414
                                                                                                                                                                                  ----VCAAGFQGNGTICTAINACEISNGGCSAKADCKRTTPGRRVCTCKAGYTGDGIVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                 GFNGTACELCWHGRFGPDCQPRSCSEHGQCDEGITGSGECLCETGWTAASCDTPTAVFAV 915
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                                                                                        VTGAIALAAYSYFRLKQRTTGFQRFDQKRTLMSWLLAS-----SSPRISQTLCMRPQRR 1388
                                                                                                                                   LSIRGTLEVPQNSGLPGNKSLSGRDIEHHLTNVNVSFYNDLVNGTFLRTMLGSQLLITTFS 1275
                                                                                                                                                                                                                                                                                                                          NQLSYAQKAKYHLCSAGWLESGRVAYPTTYASQKCGANVVGIVDYGSRANKSEMWDVFCY 1155
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-PSYDPFTDSE
                            HPQSPPVTPSQ 1399
                                                           VTGAVALAAYSYFRINRRTIGFQHFESEEDINVAALGKQQPENISNPLYESTTSAPPE--
                                                                                                                                                                                  LSIRGTLEVPQNSGLGENETLSGRDIEHHLANVSMFFYNDLVNGTTLQTRLGSKLLITAS
                                                                                                                                                                                                                                               RMKDVNCTCKVGYVGDGFSCSGNLLQVLMSFPSLTNFLTEVLAYSNSSARGRAFLEHLTD 1193
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US-60-230-445-1388; Sequence 1388; Appli; GENERAL INFORMATION:

Application US/60230445

APPLICANT: Beasley, Ellen TITLE OF INVENTION: ISOLAY TITLE OF INVENTION: NUCLE TITLE OF INVENTION: AND U

ISOLATED HUMAN TRANSPORTER PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN AND USES THEREOF

TRANSPORTER PROTEINS

FILE REFERENCE:

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SOFTWARE: FastSEQ for
SEQ ID NO 1388
LENGTH: 1895
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CURRENT FILING DATE: 2000-09-06
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nes 912; Conserv
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                                                                                                                                                                                                   FHVIRDSKALASDLPRSASWKTLQGSELSVRCGTGSDIGELFLNEQMCRFIHRGLLFDVG 736
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                                                                                                                                  VAYGIDCLLMNPTLGGRCDTFTTFDIPGECGSCIFTPKCPLKSKPKGVKKKCIYNPLPFR 796
                                                                                                                                                                                                                                                YIKESNLIQDSGLLSVITDPIHTPVTLEWPTDQALHALPAEQQDFLFNQDNKDKLKEYLK
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                                                RNVEGCQNLCTVVIQTPRCCHGYFMPDCQACPGGPDTPCNNRGMCRDLYTPMGQCLCHTG 856
                                                                                                                                                                                    FHVIRDAKVLAVDLPTSTAWKTLQGSELSVKCGAGRDIGDLFLNGQTCRIVQRELLFDLG
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               FNGTACELCWHGRFGPDCQPRSCSEHGQCDEGITGSGECLCETGWTAASCDTPTAVFAVC
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65.6%; Pred. No. 0;
vative 105; Mismatches
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Sequence 63, Application PC/TUS0113403
GENERAL INFORMATION:
APPLICANT: WEIGEL, PAUL H.
APPLICANT: ZHOU, BIN
APPLICANT: WEIGEL, JANET A.
TITLE OF INVENTION: IDENTIFICATION AND USES OF
FILE REFERENCE: 618754/JP/199,538
CURRENT APPLICATION NUMBER: PCT/US01/13403
CURRENT FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 60/245.320
PRIOR FILING DATE: 2000-01-02
PRIOR FILING DATE: 2000-0199,538
PRIOR FILING DATE: 2000-04-25
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SEQ ID NO 63
LENGTH: 1069
TYPE: PRT
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LEINPCLENHGGCDRNAECTQTGPNQAVCNCLPKYTGDGKVCSLINVCLTNNGGCSPFAF 435
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Pred. No. 0;
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                                                             VTGAIALAAYSYFRLKQRTTGFQRFDQKRTLMSWLLAS-----SSPRISOTLCMRPQRR 1388
                                                                                            LSIRGTLEVPQNSGLPGNKSLSGRDIEHHLTNVNVSFYNDLVNGTFLRTMLGSQLLITFS 1275
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                       HPQSPPVTPSQ
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                                              VTGAVALAAYSYFRINRRTIGFQHFESEEDINVAALGKQQPENISNPLYESTTSAPPE--
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RESULT 8 PCT-US01-13403-64

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: WEIGEL, PAUL H.
APPLICANT: ZHOU, BIN
APPLICANT: WEIGEL, JANET A.
APPLICANT: WEIGEL, JANET A.
TITLE OF INVENTION: IDENTIFICATION AND USES OF A HYALURONAN RECEPTOR
FILE REFERENCE: 618754/JP/199,538
CURRENT APPLICATION NUMBER: PCT/US01/13403
CURRENT FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 60/245,320
PRIOR APPLICATION NUMBER: 60/245,330
PRIOR APPLICATION NUMBER: 60/199,538
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NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.1
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GIVHIIDKLLSPKNLLITPKDNSGRILQNLTTLATNNGYIKFSNLIQDSGLLSVITDPIH 120
                                                                                                                                                                                                              EGDGITCTVVDFCKQNNGGCAKVAKCSQKGTQVSCSCKKGYKGDGYSCIEIDPCADGVNG
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                                                                                       VAYPTTYASQKCGANVVGIVDYGSRANKSEMWDVFCYRMKDVNCTCKAGYVGDGFSCSGN 1178
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                                                                       VAYPTAFASQNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNCTCKVGYVGDGFSCSGN
                                                                                                                                        DTTVGVFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYAQKAKYHLCSAGWLETGR
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GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
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Best Local :
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LENGTH: 2157
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TYPE: PRT
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                                                                                                                                                                           VCVCKAGYTGDGIVCLEINPCLENHGGCDRNAECTQTGPNQAVCNCLPKYTGDG-KVCSL
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 SLRLLEYKELKGDGPFTIFVPHADLMSNLSQDELARIRAHRQ-----LVFRYHVVGCRRL
                                  QLQEHAVRELAGPGPFTVFAP---LSSSFNHE--PRIKDWDQQGLMSQVLRYHVVGCQQL
                                                                    TCTCQDGYMGDGELCQEINSCLIHHGGCHIHAECIPTGPQQVSCSCREGYSGDGIRTCEL
                                                                                                                                                                                                                                                            {\tt NGTCHTSANCLLDPDGKASCKCAAGFRGNGTVCTAINACETSNGGCSTKADCKRTTPGNR}
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US-09-466-778-2

Sequence 2, Application US/09466778 GENERAL INFORMATION:

APPLICANT: Hastings, Gregg et al.
TITLE OF INVENTION: Novel Hyaluronan-Bind:
FILE REFERENCE: PF487
CURRENT APPLICATION NUMBER: US/09/466,778
CURRENT FILING DATE: 1999-12-20
EARLIER APPLICATION NUMBER: 60/113,871
EARLIER FILING DATE: 1998-12-23

Hyaluronan-Binding

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                               AIALAAYSYFRLKQRTTGFQRF
                                                                                                                            NEGFVDNMTLSGPNLELHASNATLLSAN-ASQGKLLPAHSGLSLIISDAGPDNSSWAPVA
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                                                              PGTVVVSRIIVWDIMAFNGIIHALASPLLAPPQPQAVLAXEAPPVAAGVGAVLAAGALLG
                                                                                           DG----RSILQWDIIAANGILHIISEPLRAPP----TAATAAHSGLGTGIFCAVVLVTG 1337
                                                                                                                                                        NSGLPGNKSLSGRDIEHHLTNVNVSFYNDLVNGTFLRTMLGSQLLITFSQDQLHQETRFV 1286
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; ORGANISM: Homo sapiens
US-09-466-778-2
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                                                                                                                                                                                                                    LPPDRQAWLYHEDHRDKLAATLRGHMIRNVEALASDLPNLGPLRTMHGTPISFSC-SRTR 1419
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PCT-US01-13403-60
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                                                                                                                                                               Matches
                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/245,320
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: 60/199,538
PRIOR FILING DATE: 2000-04-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: WEIGEL, JANET A.
TITLE OF INVENTION: IDENTIFICATION AND USES OF A HYALURONAN RECEPTOR
FILE REFERENCE: 618754/JP/199,538
CURRENT APPLICATION NUMBER: PCT/US01/13403
CURRENT FILING DATE: 2001-04-25
CURRENT FILING DATE: 2001-04-25
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                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.1
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                                                                                 LLQQLDLVPAFSLFRELLQHHGLVPQIEAATAYTIFVPTNRSLE
RHHVVLGEALSMETLRKGGHRNSLLGPAHWIVFYNHSGQPEVNHVPLEGPMLEAPGRSLI 137
                                   RYHVVLGEKLLKNDLHNGMHRETMLGFSYLLAFFLRNDQLYVNEAPINYTNVATDKGVIH 124
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                                                                                                                                                          35.7%; Score 2810; DB 1; ilarity 40.0%; Pred. No. 7.5e-199; Conservative 222; Mismatches 546;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LITPKDALGRVLQNLTTVAANHGYTKFSKLIQDSGLLSVITDSIHTPVTVFWPTDKALEA
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                                                                                                                                                         SDAMCTDQHFQEKRAGVFHLQATSGPYGLNFSEAEAACEAQGAVLASFPQLSAAQQLGFH
                                                                                                                                                                                                                                                                                            IDPCADGVNGGCHEHATCRMTGPGKHKCECKSHYVGDGVDC-EPEQLPLDRCLQDNGQCH 1047
                                                                                                                                                                                                                                                                                                                                                                      GNSCECSLGYEGDGRVCTVADLCQDGHGGCSEHANCSQVGTMVTCTCLPDYEGDGWSCRA 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AFGPHCQACRCTVHGRCDEGLGGSGSCFCDEGWTGPRCEVQLELQPVCTPPCAPEAVCRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RFGPDCQPRSCSEHGQCDEGITGSGECLCETGWTAASCDTPTAVFAVCTPACSVHATCTE 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   {\tt TTWKPSCCPGHYGSECQACPGGPSSPCSDRGVCMDGMSGSGQCLCRSGFAGTACELCAPG}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIQTPRCCHGYFMPDCQACPGGPDTPCNNRGMCRDLYTPMGQCLCHTGFNGTACELCWHG
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                                                                                                  LCSAGWLESGRVAYPTTYASQKCGANVVGIVDYGSRANKSEMWDVFCYRMKDVNCTCKAG
                                                                                                                                                                                                          PDASCADLYFQDTTVGVFHLRSPLGQYKLTFDKAKEACAKEAATIATYNQLSYAQKAKYH 1107
                                                                                                                                                                                                                                                              RNPCTDGHRGGCSEHANCLSTGLNTRRCECHAGYVGDGLQCLEESEPPVDRCLGQPPPCH 1082
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YVGDGFS-CSGNLLQVLMSFPSLTNFLTEVLAFSKSSARGQAFLKHLTDLSIRGTLFVPQ 1226
                                                      LCLMGWLANGSTAHPVVFPVADCGNGRVGVVSLGARKNLSERWDAYCFRVQDVACRCRNG
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Best Local Sin
Matches 560;
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NUMBER OF SEQ ID NOS: 64
SOFTWARE: PATENTIN VEr. 2.1
SEQ ID NO 61
LENGTH: 1458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 61, Application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: WEIGEL, PAUL H.
APPLICANT: ZHOU, BIN
APPLICANT: WEIGEL, JANET A.
APPLICANT: WEIGEL, JANET A.
TITLE OF INVENTION: IDENTIFICATION AND USES OF A HYALURONAN RECEPTOR FILE REFERENCE: 618754/JP/199,538
CURRENT APPLICATION NUMBER: PCT/USO1/13403
CURRENT FILING DATE: 2001-04-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/245,320 PRIOR FILING DATE: 2000-11-02 PRIOR APPLICATION NUMBER: 60/199,538
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  INVCLTNNGGCSPFAFCNYTEQDQRICTCKPDYT-GDGIVCRGSIYGELPKNPSTSQYFF
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                                                                                                                                            NGTCHTSANCLLDPDGKASCKCAAGERGNGTVCTAINACETSNGGCSTKADCKRTTPGNR 360
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                                                                         VCVCKAGYTGDGIVCLEINPCLENHGGCDRNAECTQTGPNQAVCNCLPKYTGDG-KVCSL 419
                                                                                                                                                                                               GFHGTACEVCELGRYGPNCTGVCDCAHGLCQEGLQGDGSCVCNVGWQGLRCDQKITSPQC
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                                      TCTCQDGYMGDGELCQEINSCLIHHGGCHIHAECIPTGPQQVSCSCREGYSGDGIRTCEL
                                                                                                                   PRKCDPNANCVQDSAGASTCACAAGYSGNGIFCSEVDPCAHGHGGCSPHANCTKVAPGQR
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tive 220; Mismatches
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RESULT 13
US-09-715-417A-16
; Sequence 16, Application US/09715417A
; GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/166,336
PRIOR FILING DATE: 1999-11-19
PRIOR APPLICATION NUMBER: 60/167,785
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: 60/187,844
PRIOR APPLICATION NUMBER: 60/187,844
PRIOR APPLICATION NUMBER: 60/187,844
PRIOR APPLICATION NUMBER: 60/187,844
PRIOR FILING DATE: 2000-03-08
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 16
US-09-715-417A-12
US-09-715-417A-12
Sequence 12, Application US/09715417A
GENERAL INFORMATION:
APPLICANT: Shimkets, Richard
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Best Local Similarity 78.8
Matches 471; Conservative
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APPLICANT: Shimkets,

Richard

Lichenstein,

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APPLICANT: Vernet, Corine
APPLICANT: Fernandes, Elma
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACI
FILE REFERENCE: 15966-606
CURRENT APPLICATION NUMBER: US/09/715,417A
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/166,336
PRIOR APPLICATION NUMBER: 60/167,785
PRIOR APPLICATION NUMBER: 60/167,785
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR PRIOR PRIOR ONTE: 1999-11-29
PRIOR FILING DATE: 2000-03-08
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.1
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Sequence 2725, Application ....
Sequence 2725, Application ...
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, I
TITLE OF INVENTION: Nucleic Acids,
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Best Local
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PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2820
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2725
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Best Local Similarity
Matches 430; Conserv
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GSTAHPVVFPVADCGNGRVGIVSLGARKNLSERWDAYCFRVQDVACRCRNGFVGDGISTC
                GRVAYPTTYASOKCGANVVGIVDYGSRANKSEMWDVFCYRMKDVNCTCKAGYVGDGFS-C
                                                                                                                                                              GGCHEHATCRMTGPGKHKCECKSHYVGDGVDC-EPEQLPLDRCLQDNGQCHPDASCADLY 1056
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                                                                                                      FQDTTVGVFHLRSPLGQYKLTFDKAKEACAKEAATIATYNQLSYAQKAKYHLCSAGWLES
                                                                                                                                           GGCSEHANCLSTGLNTRRCECHAGYVGDGLQCLEESEPPVDRCLGQPPPCHSDAMCTDLH
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                                                                      FQEKRAGVFHLQATSGPYGLNFSEAEAACEAQGAVLASFPQLSAAQQLGFHLCLMGWLAN
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US-60-360-039-6445 US-10-123-155-37
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US-09-970-944-32
PCT-US02-08253-216
US-09-766-511B-29

ALIGNMENTS

; ORGANISM: homo sapiens US-10-123-962-2 Sequence 2, Application US/10123962 GENERAL INFORMATION: APPLICANT: Friddle, Carl Johan NUMBER OF SEQ ID NOS: 5 SOFTWARE: FrastSEQ for Windows Version 4.0 SEQ ID NO 2 LENGTH: 1986 Query Match 77.2 Best Local Similarity 77.0 Matches 1083; Conservative FILE REFERENCE: LEX-0338-USA CURRENT APPLICATION NUMBER: US CURRENT FILING DATE: 2002-04 PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 2001-04-24 APPLICANT: Gerhardt, Brenda APPLICANT: Zambrowicz, Brian TITLE OF INVENTION: Novel Human EGF-Family Proteins 1 SLPSLLTRLEOMPDYSIFRGYIIHYNLASAIESADAYTVFVPNNEAIENYIREKKATSLK 60 77.2%; 77.0%; 2002-04-16 121; US/10/123,962 60/286,141 Score 6072; Pred. No. 0; Mismatches No. DB 6; 191; Length 1986; and Indels Polynucleotides Encoding 12; Gaps 5

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APPLICANT: Gerhardt, Brenda
APPLICANT: Zambrowicz, Brian
TITLE OF INVENTION: Novel Human EGF-Family F
FILE REFERENCE: LEX-0338-USA
CURRENT APPLICATION NUMBER: US/10/123,962
CURRENT FILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: US 60/286,141
PRIOR PILING DATE: 2001-04-24
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
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Best Local Similarity
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RESULT 3
US-10-104-047-2580
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APPLICANT: HELIX RESEARCH INSTITUTE TITLE OF INVENTION: NOVEL full length FILE REFERENCE: H1-A0105
                                                                                                                                                      NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2580
LENCTH: 510
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/104,047 CURRENT FILING DATE: 2002-03-25 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                  PRIOR FILING DATE:
                                                                                                                   ORGANISM: Homo
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PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3794, Application US/10104047 GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/104,047 CURRENT FILING DATE: 2002-03-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 482
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FLKHLTDLSIRGTLFVPQNSGLPGNKSLSGRDIEHHLTNVNVSFYNDLVNGTFLRTMLGS
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                                                                                                                                                              ATIATYNQLSYAQKAKYHLCSAGWLESGRVAYPTTYASQKCGANVVGIVDYGSRANKSEM 1149
                                                                                                                                                                                                                                                                                             VTCTCLPDYEGDGWSCRARNPCTDGHRGGCSEHANCLSTGLNTRRCECHAGYVGDGLQCL
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                                                            WDAYCFRVQDVACRCRNGFVGDGISTCNGKLLDVLAATANFSTFYGMLLGYANATQRGLD
                                                                                                WDVFCYRMKDVNCTCKAGYVGDGFS-CSGNLLQVLMSFPSLTNFLTEVLAFSKSSARGQA 1208
                                                                                                                                      AVLASFPQLSAAQQLGFHLCLMGWLANGSTAHPVVFPVADCGNGRVGVVSLGARKNLSER
                                                                                                                                                                                                                 EESEPPVDRCLGQPPPCHSDAMCTDLHFQEKRAGVFHLQATSGSYGLNFSEAEAACEAQG
                                                                                                                                                                                                                                                     EPEQLPLDRCLQDNGQCHPDASCADLYFQDTTVGVFHLRSPLGQYKLTFDKAKEACAKEA 1089
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Pred. No. 2.3e-35;
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US-60-360-039-5280
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SEQ ID NO 5280
LENGTH: 1111
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cao, Yongwei
APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry
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                                                                                                     HGG-CDRNAECTQ-----TGPNQAVCNCLPKYTGDGKVCSLINVCLTNNGG--CSPFAFC 436
                                                                                                                                                        DIGCSRGRFGLQCKQNCTCPGLEFSDSNASCDAKTGQCQCESGYKGP--KCDERKCDAEQ
                                                                                                                                                                                                                                                                                                                     QNGGKCNK----EGKCVCSDGWGGEFCLNKCEEGKFGAECKFE-----CN--CQNGATC-
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DWNHASECNPETGSCVCKPGRTG---
                                   NYTEQDQ-----RICTCKPDYTGDGIVCRGSIYGELPKNPSTSQYFFQLQEHAVRELAGP 491
                                                                                                                                                                                               --GCST---KADCKR--TTPG-------NRVCVCKAGYTGDGIVCLEINPCLEN
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                                                                              YGADCSKTCTCVRENTLMCAPNTGFCRCKPGFYGDN--CEL--ACSKDSYGPNCEKQAMC
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Hinkle, Gregory J.
Slater, Steven C.
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••	aps 74;	3507; s 932; G	7; Length 14; 490; Indel	core 399; DB red. No. 3.8e- Mismatches	18; S 78; P 153;	sch 5 al Similarity 16 316; Conservative	2 =	Query Ma Best Loc Matches	
ON OF	PRODUCTION	PLANTS FOR I	PROTEINS IN PROPERTIES	0039 MICROBIAL IMPROVED PP /360,039)3()76(21	-5784 -5784 -5784 -5784 -5784 -5784	GUT 6 60-360-039 60-360-039 equence 57 eneral in papelicant: Appelicant: Appelicant: Appelicant: Appelicant: Tiple OF if OUNRENT OF LEGITH: ORGANISM: ORGANISM:	APPLICA ITILE O TITLE RE CURRENT CURRE	g
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		1079	RSPLGQYKLTFD	YFQDTTVGVFHL-	PDASCADL	EPEQLPLDRCLQDNGQCHPDASCADLYFQDTTVGVFHL	30	10	Qγ
	861	: : CPESTFGLKC	: : PGFTGEFCHAL	SCNRVSGACHCHPGFTGEF	: : CKCQGTAT	DKPCEDGYYGPDCIKKCKCQGTATSSCNRVSGACHCHPGFTGEFCHALCPESTFGLKC	0.4	60 40	g 49
	803	PAGFQGDRC	CNAQTGECSCP	RQVCR	SAGFWGNG	ICPAGLE GALCTRPC	48	7	Db Db
	986	ξĐ	VSCSCK	ITCTVVDFCKQNNGGCAKVAKCSQKGTQVS	FCKQNNGG 	CVCNLNYEGDGITCTVVD	32	9	Qy
	931 747	/HATCTE-NNT : 	AVCTPACSVHATCTE- : : : GCALDCPKCASGSTCDHI	TPTAVF	CETGWTAA : CEPGYHGK	SEHGQCDEGITGSGECLCETGWTAASCD- :- : :- PTTGECICEPGYHGKTCSE	79 C 91 C	6 8	Qy Db
	878 690	RFGPDCQP-RS : !YGDGCQQVCS	TACE-LCWHGR	GQCL-CHTGFNGTACE-LCWHGRFGPDCQP-RS	PCASTDPK	PCNNRG-MCRDLYTPMGQCL-CHTGFNGTACE-LCWHGRFGPDCQP-RS	34 31	on 10	Qy Db
	630	ACPGGPDT	GYFMPDCQACP		CQNLC : CELSCPCS	VKKKCIYNPLPFRRNVEGCQNLC	95	5 7	Qy Db
	594	CSTTCSKGK-	PG	GEC	HCKCVNGK	ດ	42 AN	Ол ~	Db
	793	DFITGECTCFAGEQG	520	CADALLA IDONALA I TONO TONO CANCENACIÓN CON CANCENACIÓN CON CANCENACIÓN CON CANCENACIÓN CON TIMENTE CON CANCENACIÓN CON CANCEN	Wilder COR	;		J U	200
	730	EQMCRFIHRG	GSDIG-ELFLNEQMC	T	RS	SD	ĸs	1 (5)	y Qy
	510			HCPADTF			00 RCEH	υı	dd
	671	'LFNQDNKDKL	LEALPPEQQDF	KFSKLIQDSGLLSVITDSIHTPVTVFWPTDKALEALPPEQQDFLFNQDNKDKL	LSVITDSI	AANHGYTKFSKLIQDSGLI	12 AAI	6	Qy
	499	PRUALGRYLQNLTIV : : GADGKCQCDRGWTGH	KNULLTPRUAD GADGK	SDIISTNGVIHVIDKLESPKNEELITPKDAEGKVEQNEIT ; ; GADGKCQCDRGWTGH	LSSULIST	LSVSQUTVEINNEAKVLS	85	ט ב	дд QУ
	484		D	VGCD-	CNORG	PLDFYGPNCAHQCQC-	1 C	4 1	Db
	100	TORTILLOGER	VGCQQLLLDNLKVITSATTLQGEF - -	LIII THISQVERYHVYGC	: : : : :	GPFTVFAPLSSSFNHEPRIKDWDQQGLMSQVLRYHV	492 GP)		Qy

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134 KNRCDNNDTIIVRGECGKCSQQAPCPLET-KPLRETRKCIYSIYEMGKRSVFIGCQP--Q 190

21	O WPTSYSTIASETEATTANTOROUTTOTTOTTOTTOTTOTTOTTOTTOTTOTTOTTOTTOTT	2572	B
581	KDK	663	Qy
2571	TTASETSEPLTEDSLTVSVRIHELTTSSENVPKESESTTTSSESSKPSQEPAGILTSTVV 2	2512	DЪ
62	DKALEALPPEQ	648	Qy
2511	LSESSTTPESSSKSPVSSSTEGISVVTSTEFSK-VPESTISSVLEEDLTKTTPSPILEET	2453	Db
547		616	Оу
2452	DV	2393	ф
515	SPKNLLITPKDALGRVLQNLTTV	589	Qy
2392	TEAPTTLSPDILSTTINNLSQSSTVSTEDRSEISSENSEKPTSAPELVTSSVTHVASSSP 2	2333	Db
588	DIIST	573	Qy
2332		2273	ДЪ
572	SISVSQDTVFINNEAKVL	553	Qy
2272		2213	Дb
552	LMSQVLRYHVVGCQQLLLDNLKVTTS	518	Qy
2212		2153	Db
517		506	Qy
2152	SSVKSSPSTPSTTSQSVTSTVPETSKSTVLSSEAPVTSTSPTEVHTSSETKPSLSASSTT 2	2093	DЬ
505	HAVRELSGPGPFTVFAPLS	483	Qy
2092	ETTVSSTPSESSSEAPLTSSPATTTEVITESSVKSTTPKEESSSEITVKLSSKSPEVT	2033	Db
182		455	Qy
2032	VSSTSATSSESTTAEPHVTTSISSTTSTKDMTSSKSPENVTMSSESPEVSTSSSKSTTAS 2	1973	DЬ
154	6 4	455	Qy
1972	. 4	1913	Db
154	TEQDQRICTC	439	Qy
1912	LCAQK	1860	DЪ
138	GGCDRNAECTQTGPNQAVCNCLPKYTGDGKVCSLINVCLTNNGGCSPE	386	Qy
1859	TKIEEEPKSDKTACTDEWSRLCELEKKQCTVDEEEVPQCGACLPGHHPINGTCQSLQISG 1	1800	Db
385		376	Qy
1799	GSYRCECAEGYEGEGGVCTDIDECDRGMAGCDSMAMCINRM-GSCGCKCMAGYTGDGATC	1741	Db
375	GKASCKCAAGFRGNGTVCTAINACETSNGGCSTKADCKRTTPGNRVCVCKAGYTGDGIVC	316	Qy
1740	VSCLSVRIYNGSL-SSVCECEPGFRFEKESNSCVDIDECEESRNNCDPASAVCVNTE 1	1685	Db
315	-SCVHGRCSQGPLGDGSCDCDVGWRGVKCDMEITTDNCNGTCHTSANCLLDPD	264	Qy
1684		1625	DЪ
263	TACETCTEGKYGIHCDQAC	245	Qy
1624	CVAEKAPCSLNANCVNMNGTFSCSCKQGYRGDGFMCT	1588	DЬ
244	CVRTIITRACWLASLAHNAKPAPGEVKMCALGTASVW	191	Qy
1587	KKPCDSTQSSKSHCSESNMSCEVDTVDGSVECKECMGGYKKSGKVCEDINE	1537	DЪ

		ORGANISM: Caenorhabditis elegans	ORGA	٠. ،
		TH: 1584		
		APPLICATION FILING DATE F SEQ ID NC	- M R R	
OF	PRODUCTION	INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR INVENTION: PLANTS WITH IMPROVED PROPERTIES ERENCE: 38-10(52052)A	TITLE OF I TITLE OF I FILE REFER	*. *. *. *
		CANT: GOLdman, Barry S. CCANT: Hinkle, Gregory J. CANT: Slater, Steven C.	APPLICANT:	
		Chen, Xianfeng	APPLI	
		6549, App.	Sequ	
		39	-00-	RE
		8 QGKLSVYCEADGMTLVLGNETADFEGKLFVK 3308	327	Db
		1 QVLMSFPSLTNFLTEVLAFSKSSARGQAF	, 118	Qy
	27	9 ETCADIDECAEKSHKCDRVATCRNTFGSHVCTCPDGHVGDGITC	32	Db .5
	_	NOSOSSOCIONAS SENTINOS MESOS ANTERES ANTES SANTAS S		Q 2
	3228	FKGDPFYKCSSLVSKEPANQQDLSDVSSCVTPCDSSTQLCISGECICK		Дb
	1127	YK-LTFDKAKEACAKEAATIATYNQLSYAQKAKYHLO	1074	Qy
	3168	9	312	Db
	1073	0	, 102	Qу
	3128		3077	Db
	1019	AKCSQKGTQVSCSCKKGYKGDGYSCIEIDPCADGVNGGCHEH	962	QΥ
	3076	: YVCSPHPQDCVLRDN	3020	Db
	961	.2 VFAVCTPACSVHATCTENNTCVCNLNYEGDGITCTVVDFCKQNNGGCAKV	, 912	Qy
	3019	3 FIGDGTTACSKKSTADCISLPSLCADKAKCDNSTRSCECDAGYIGDG	297	Db
	911	7 FNGTACELCWHGRFGPDCOPRSCSEHGQ	, 85	QΥ
	2972	0 TNQEEEQVTSTTTTEAPSLCSTVTCHSLATCEQSTGVCICRDG	293	Db
	856	7 RNVEGCONLCTVVIQTPRCCHGYFMPDCQACPGG	, 79	Qy
	2929		287	Db
	796	8 SCIFTPKCPLKS	, 76	Qy
	2869	.0 VTASSIPSEEPILSSVTSSSTPRVRLITGTPDDLIVSVTVPSHGNRRQNITASSVPSNST	2810	рb
	767	MN	~1	Qy
	2809	:	275	DЬ
	735	VRCGTGSDIGELFLNEQMCRFIHRGLLF	706	Qу
	2751) STENVETSTSOSGSLESSTMSSTSSEPETNAPAVTVSSEASSTTLEENSSTSSPTSSEAS	269	Db
	705	2DSKALASDLPRS	, 68	Qy
	2691	32 VSTTVSTTTPTEETTTSESLILTAAPSKPTESTTESSEAPTTPAKTSETKPSNVSSTSRK	263	Db
	681	32	, 68	Qy

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                                                                      DTP--CNNRGMC-RDLYTPMGQCLCHTGF--NGTACELCWHGRFGP---DCQPRSCSEH
                                                                                                       HCVINE-
                                                                                                                                  KCIYNPLPFRRNVEGCQNLCTVVIQTPRCCHGYFMPDCQACPG-------
                                                                                                                                                                                                                                                    KDKLKSYLKFHVIRDSKALASDLPRSASWKTLQGSELSVRCGTGSDIGELFLNEQMCRFI
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-DEGITGSGECLCETGWTA---ASCD---TPTAVFAVCTPACSVHATCTENNT-
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20.2%;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 193;
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TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10($2052)A

CURRENT APPLICATION NUMBER: US/60/360,039

CURRENT FILING DATE: 2002-02-21
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                                                                                                                                                             NKDGTFECLCKDGYEGDPSSECRDVNEC-KNPDACGPNSQCTNTQGGYE-CECLAGFERI
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                                     STSQYFFQLQEHAVRELAGPGPFTVFAPLSSSFNHEPRIKDWDQQGLMSQVLRYHVVGCQ 531
                                                                              AEGAHCTDRDECAVE - - PCHPAAICSNTRGSYK - CECRDGFVGDGKTCHE - - -
                                                                                                                 GDGKVCSLINVCLTNNGGCSPFAFCNYTEQDQRICTCKPDYTGDGIVCRGSIYGELPKNP 471
                                                                                                                                                                                                {\tt TTPGNRVCVCKAGYTGD-GIVCLEINPCLENHGGCDRNAECTQTGPNQAVCNCLPKY--T}
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Hinkle, Gregory J.
Slater, Steven C.
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19.3%; Pred. No. 2.9e-13;
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TILYPISNDSTVIPR--SWD-
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 5866
LENGTH: 3051
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US-60-360-039-5866
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                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 244; Conserv
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                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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                                                                                                                                                                                                    4.7%; Score 371; DB 7; Length 3051; ilarity 20.4%; Pred. No. 1.2e-12; Conservative 109; Mismatches 427; Indels 41
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ATGAQSYTCECLSGYADRSPD--PRNKPGRLCVLTEPVCLDPEQNDCHAAAICSEV 1870
                                     MTGPGKHKCECKSHYVGDGVDCEPEQLPLDRCL-----QDNGQCHPDASCADL 1055
                                                                                                                          KCSQKGTQVSCSCKKGY--
                                                                                                                                                                     CPPNHDCSSAAVCEPLGGMKYQCVCIQGYVDQSPGSQKGRVCVRNNACHDPRLNTCSRNA 1756
                                                                                                                                                                                                             CTP--ACSVHATCTE----NNTCVCNLNYEGDGITCTVVDFCKQNN------GGCAKVA 962
                                                                                                                                                                                                                                                       R------HTCSSHADCRDLEEGYT----CECRDGYVDRSPNLASQPGRVCSAP----EV 1696
                                                                                                                                                                                                                                                                              RFGPDCQPRSCSEHGQC---DEGITGSGECLCETGWTAAS---
                                                                                                                                                                                                                                                                                                                                            NECESGVHDCDPSATCRDNEQSFT----CECPSGFVDRSPNKHARPGRVCVKLVDECREG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTLG--GR-CDTFTTFDIPGECGSCIFTPKCPLKSKPKGVKKKC-----IYNPLP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CQCRDGFKDIGDRRRPGRMCKPMVNE--CQYPHLNDCHQNAACIDLEEGYECKCNQGFMD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CSPNADCIDTPES----YKCRCRDDFVDESPDSSRRPGRI-----CRPALVDECRTGK 1306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGPGPFTVFAPLSSSFNHEPRIKD------WDQQGLMSQVLRYHVVGCQQLLLDNLKVTT 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TDTE-DSYICACPQSHIDLSPDTVNRPGRRCLMRI-----NECTSN------RHD 1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NYTEQDQRICTC-----KPDYTG-DGIVCRGSIYGELPKNPSTSQYFFQLQEHAVREL 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DDCARDGGICEDNPDSFTCRCAMNYLDVSFDRVTRPGRKCKRLINECQTGQNDCSEEATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLNDCDSPD-----RAVCTDTDDG-YMCRCRQGFLDISPSISVKPGRLCKPLQNECALGI 1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IKTNDKCSPGKNDCDRNARCIQIGDDDYSCACPPGFKDKSPSSSRPGRLCIPVIPECDNP 1100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VCKELVNECTNPRLN-QCDRNAHCI-----DTIEGYSCICKPGFVDMDEFGNPGRRCEQ 1040
                                                                                  ICYDEPRGYRCECKRGFMDRSPDSSQRGRVCEPPPPPSPPPRHPCQDPERNDCHPAGTCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSHGRPGRICKQLTNECLRPSLNSCDRNARC--IDKEEGYECECRDGFIDVSPSPTLKGR 1539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VRCGTG-SDIGEL-----FLNEQMCRFIH-----RGLLFDVGVAYGIDCL--LMN 747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---DALGRVLQNLTTVAANHG------YTKFSKLIQDSGLLSVITDSIHTPVTVFW 645
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                                                                                                                          --- KGDGYSC
                                                                                                                        -IEIDPCADGVNGGCHEHATCR 1007
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Best Local Similarity
Matches 254; Conserv
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SEQ ID NO 5971
LENGTH: 1372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KPGYTGPRCD--VKQDQCADSPCLNDAQC-VDMGGAYKCVCKSGWTG-----PKCEQ 255
                                                                                                                               QHCQRSEEIYKGLLVRFEGFTKIIGRVERTHKSTCGVEEKSAMQKSQSQILIEDCPSDMV
                                                                                                                                                                                                                  TYSNNGYATGKQLDVMTG-----ITLGSTALPSFVGSIARVGVWNRVIDFEEEL--PLMV
                                                                                                                                                                                                                                                            VTTSATTLQGEPVSISVSQDTVFINNEAKVLSSDIIST-----NGVIHVIDKLLSP---
                                            IS-SMDRETNVTWPEPTFLSSNSKIEKIEKNLKQGQMFTWGEYDVLYTATDNATNQAQCN 696
                                                                                       ITDSIHTPVTVFWP----TDKALEALPPE---
                                                                                                                                                                                                                                                                                                     LTLFPGLAAVEVPLSSSQHLNNGKWNH--LLITWQSK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ----CRGSIYG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---CVCKAGYTGDGIVCLEINPC-LENHG--GCDRNAECTQTGPNQAVCNCLPKYTGDGK 415
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                                                                                                                                                                     ---KNLLITPK---DALGRVLQNLTTVAANHGYTKFSK-----LIQDSGLLSV 632
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LPRSASW-KTLQGSELSVRCGTGSDI--
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                                                                                  -----QQDFLFN-QDN-KDKLKSY
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; ORGANISM: Homo PCT-US02-09671-697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US02-09671-697 ; Sequence 697, Application PC/TUS0209671
                                                                                                                                                                           PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: 60/29
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/31
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/32
PRIOR APPLICATION NUMBER: 60/32
PRIOR FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: 60/32
PRIOR FILING DATE: 2001-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Zycos Ir
                                                                             SEQ ID NO 697
                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: PCT/US02/09671
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/279,495
                                                                                                NUMBER OF SEQ ID NOS: 2041
SOFTWARE: FastSEQ for Windows
                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 08191-026WOI
                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: TRANSLATIONAL PROFILING
                                                                                                                                      PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2002-02-20
                                                      LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLYTPMGQCLCHTGFNGTACELCWHGRFGPDCQPRSCSEHG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -NLCTVVIQTPRCCHGYFMPDCQACPGGPDTPCNNR-----
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                                                                                                  Version
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Query Match
Best Local Similarity
Matches 101; Conserv

Conservative

4.3%; Score 338; DB 1; Length 3494; 31.4%; Pred. No. 9.6e-11; tive 30; Mismatches 125; Indels 6

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PCT-US02-09671-703
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                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version SEQ ID NO 703
                                                                                                                                                                                                                                                                       Matches 101;
                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: PCT/US02/09671
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/279,495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Zycos Inc.
TITLE OF INVENTION: TRANSLATIONAL PROFILING
FILE REFERENCE: 08191-026W01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 60/358,985
PRIOR FILING DATE: 2002-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/326,370 PRIOR FILING DATE: 2001-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/336,780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/292,544 PRIOR FILING DATE: 2001-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-03-28
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                                                                                                                                                                                                                                                                                           Local Similarity
ETSNGGCST--KADCKRTTPGNRVC-VCKAGYTGDGIVCLEINPCLENHGGCDRNAECTQ 396
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                                      SSPNSPACTLD -- RDECSFQPGPCSTLVQC - FNTQGSFYCGACPTGWQGNGYICEDINEC
                                                                          ---RGVKCDMEITTDNCN---GTCHTSANCLLDPDGKASC-KCAAGFRGNGTVCTAINAC
                                                                                                              --SYSCH-CPPETYGPQCASKYDDCEGGSVARCVHGICEDLMREQAGEPKYSCVCDAGWM
                                                                                                                                                  FNGTACETCTEGKYGIHC-----DQACSCVHGRC----SQGPLGDGSCDCDVGW-
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Pred. No. 9.6e-11;
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: NAME/KEY: misc_feature
: LOCATION: (1757)..()
: OTHER INFORMATION: Xaa =
US-10-150-821-4
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US-10-150-821-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Welcher, Andrew A.
APPLICANT: Elliott, Gary S.
TITLE OF INVENTION: C3B/C4B COMPLEMENT RECEPTOR-LIKE MOLECULES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 01017/37592
CURRENT APPLICATION NUMBER: US/10/150,821
CURRENT FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: US/09/911,842
PRIOR APPLICATION NUMBER: US/09/911,842
PRIOR APPLICATION NUMBER: US/09/911,842
PRIOR FILING DATE: 2001-07-24
PRIOR FILING DATE: 2000-08-01
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Matches 336;
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ORGANISM: Mus musculus
FEATURE:
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DQQGLMSQVLRYHVVGCQQLLLDNLKVTTSATTL----
                                            G-----HRCETEQ-
                                                                                   GDGIVCRGSIYGELPKNPSTSQYFFQLQEHAVRELAGPGPFTVFAPLSSSFNHEPRIKDW 513
                                                                                                                                                                                                            VNECQSS--PCLNNAVCKDQV-GGFSCKCPPGFLGTR--CEKNVDECLSQ--PCQNGATC 1386
                                                                                                                                                                                                                                                      INACETSNGGCSTKADCKRTTPGNRVCVCKAGYTGDGIVC-LEINPCLENHGGCDRNAEC 394
                                                                                                                                                                                                                                                                                                CECSLGYSGQICEENI--NECISSPCLNKGTC---TDGLASYRCTCVKGYM--GVHCETD 1333
                                                                                                                                                                                                                                                                                                                                        CDCDVGWRGVKCDMEITTDNC-NGTCHTSANCLLDPDGKAS--CKCAAGFRGNGTVC-TA 335
                                                                                                                                                                                                                                                                                                                                                                                  HNSGTCQQLGRGYVCLCPPGYTGLKCET------DIDECSSLPCLNGGICRDQVGGFT 1280
                                                                                                                                                                                                                                                                                                                                                                                                          NGTGTCQ-----CGLGFNGTACETCTEGKYGIHCDQACS--CVHGRCSQGPLGDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTITGATSITDCSSFSSTFSAAEESIVPLVAPGHSQNKYEVSSQVFHECFLNPC-----
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                                                                                                                           -KDGANSFRCQCPAGFTGTH--CELNINECQSN--PCRNQATC-VDELNSYSCKCQPGFS
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Pred. No. 9.9e-11;
6; Mismatches 555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1506 TFLLTDYNGWVLYVNGKEKITNCPSVN-DGIWHHIAITWTSIGGAWRVYIDGELSDGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     846 TPMGQCL---CHTGFN--GTACELC----WHGREGPDCQPRSCS----EHG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVSGIYGYV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C---TASGSWDRAPPSCQLVSCGEPPIVKDAVITGSNFTFGNTVAYTCKEGYTLAGPDTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSKYSLFCDPGFQMYGNPVQYCLNQGQWTQPLPHCERIRCGLPPALENGFYSAEDFHAGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSIGKAIPGGGALVLGQEQDKKGEGFNPAESFVGSISQLN-LWDYVLSPQQV-----KLL
                                                                                                                                                                                                                                                                                                                                                                                           A-KFAAGSVVSFK-----CMEGFVLNTSAKIECLRGGEWSPSPLSVQCIPVRCGEPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EAATIATYNQLSYAQKAKYHLCSA--GWLESGRVAYPTTYA--SQKCGANVVGIVDYGSR 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ICQAN----GKWNSSNHQCLA-VSC-----DEPPNVDH-ASPETAHRLFGDTAFYYCA-
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  ---IIAANGILHIISEP-
                                                                                                                                                                                    NGFLEHTTGRTFESEARFQCNPGYKAAGSPVFVCQANRHWHSDAPLSCTPLNCGKPPPIQ 2297
                                                                                                                                                                                                                                                                      -AFLKHLTDLSIR-
                                                                                                                                                                                                                                                                                                            IANGYPSGTNYSFGAVVAYSCHKGFYIKGEKKSTCEATGQWSKPTPTCHPVSCNEPPKVE
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                                                            QLVLKELASEVGVMT1SCKEGHA----LQGPSVLKCLPSGQWNGSFPICKMVLCPSPPLI 2413
                                                                                                    GTFLRTMLGSQLLITFSQDQLHQETRFVDGRSIL----
                                                                                                                                            NGFLKGESFEVGSKVQFVCNEGYELVGDNSWTCQKSGKWSKKPSPKCVPTKCAEPPLLEN 2357
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-LRAPPTAATAAHSGLGTGI-FCAVV-----
                                                                                                                                                                                                                                                                      --GTLFV-----
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RESULT 15
PCT-US02-09671-701
Sequence 701, Application PC/TUS0209671
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PRIOR APPLICATION NUMBER: 60/292,544
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/310,801
PRIOR APPLICATION NUMBER: 60/310,801
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/326,370
PRIOR FILING DATE: 2001-10-01
PRIOR FILING DATE: 2001-10-01
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SEQ ID NO 698
LENGTH: 3623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 4.3%;
Best Local Similarity 31.4%;
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CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/279,495
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TITLE OF INVENTION: TRANSLATIONAL PROFILING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/358,985 PRIOR FILING DATE: 2002-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/336,780 PRIOR FILING DATE: 2001-12-04
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                                                                                                                    SGWT - - GVNCTENI - NECLSNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFGVPASSGALHFGSTVKYLCVDGFFLRGSPTILCQADSTWSSPLPECVPVECPQPEEIL 2473
                                                                                                                                                           PDYTGDGIVCRGSIYGELPKNP
                                                                                                                                                                                                                                                                                                  EINNGGCSVAPPVECV-NTPGSSHCQACPPGYQGDGRVCTLTDICSVSNGGCHPDASCSS
                                                                                                                                                                                                                                                                                                                                                                                          SSPNSPACTLD--RDECSFQPGPCSTLVQC-FNTQGSFYCGACPTGWQGNGYICEDINEC
                                                                                                                                                                                                         TLGSLPLCTCLPGYTGNGYGPNGCVQLSNICLSHPCLNGQCID-TVSGY--
                                                                                                                                                                                                                                                                                                                                           ETSNGGCST--KADCKRTTPGNRVC-VCKAGYTGDGIVCLEINPCLENHGGCDRNAECTQ 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --SYSCH-CPPETYGPQCASKYDDCEGGSVARCVHGICEDLMREQAGEPKYSCVCDAGWM
                                                                                                                                                                                                                                                      TGPNQAVCNCLPKYTGDG----KVCSLINVCLTN---NGGCSPFAFCNYTEQDQRICTCK 449
                                                                                                                                                                                                                                                                                                                                                                                                                                      --- RGVKCDMEITTDNCN---GTCHTSANCLLDPDGKASC-KCAAGFRGNGTVCTAINAC
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; Pred. No. 9.9e-11; 
30; Mismatches 125; Indels 6
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GENERAL INFORMATION:
APPLICANT: Zycos Inc
TITLE OF INVENTION:

Inc

TITLE OF INVENTION: TRANSLATIONAL PROFILING FILE REFERENCE: 08191-026W01

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CURRENT APPLICATION NUMBER: PCT/US02/09671
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/279,495
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: 60/292,544
PRIOR FILING DATE: 2001-05-21
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/310,801
PRIOR APPLICATION NUMBER: 60/326,370
PRIOR APPLICATION NUMBER: 60/326,370
PRIOR APPLICATION NUMBER: 60/36,370
PRIOR APPLICATION NUMBER: 60/36,780
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2002-02-20
NUMBER OF SEQ ID NOS: 2041
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 701
LENGTH: 3623
Search completed: June 17, 2002, 12:34:07 Job time: 313 sec
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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AA275305 vc03d11.r BE447169 ut55c09.x	T91781 yd52d09.s1	BB745695 BB745695	BI832486 603082278	BB847553 BB847553	BB735524 BB735524	BI146461 602913560	BB086042 BB086042	T47504 yb14f01.r1	BE656181 UI-M-BH0-	BB842118 BB842118	BF601840 266924 MA	BI838464 603083445	AA821602 vw30c03.r	BF401567 UI-R-CA0-	BB626584 BB626584	Description	

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	AZ487512 1M0317A17	BM148089 TCAAP1Q82	BE233224 139315 MA	BG712275 pglln.pk0	AL598662 DKFZp313N	A1606926 vw30c03.x	AZ487818 1M0317A17	A2030878 RPCI-23-3	=	BI006218 RC5-RT005	BG964207 602828983		AI272209 ap22a07.x	R97483 yq53h06.r1	BG803514 0232-46 M	AA138267 mr06b11.r	BI695595 603344723	BG383208 301171 MA		BI183898 UNL-P-FN-	BE808086 213204 MA	4	AA257161 zr82b05.r	A1852814 UI-M-BH0-	BG712246 pglln.pk0	AU080852 AU080852	BI518863 603061773

ALIGNMENTS

	TITLE JOURNAL COMMENT		ORGANISM REFERENCE AUTHORS	RESULT 1 BB626584 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp, Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Taawa,M., Ohara,E., watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and	Muramatsu,M. and Hayashizaki,Y. RIKEN Mouse ESTs (Arakawa,T., et al. 2001) Unpublished (2001) Contact: Yoshihide Hayashizaki	, Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 664) Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.	BB626584 FIKEN full-length enriched, adult male dienosphalon Musmusculus cDNA clone 9330210123 5', mRNA sequence. BB626584 BB626584 BG1:16464521 EST. house mouse.

FEATURES

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BASE COUNT
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Best Local Similarity
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Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sug
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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ,Y. and Hayashizaki,Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Computer-based methods for the mouse full-length cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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primed with a primer (5'
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/tissue_type="diencephalon"
/dev_stage="adult"
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/note="Site_1: SalI; Site_2: BamHI; cDNA library was
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="9330210123"
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/lab_host="DH10B (Life Technologies)" /note="Vector: pT7T3D-Pac (Pharmacia) with polylinker; Site_1: Not I; Site_2: Eco RI;

The UI-R-CA0

modified

/clone="UI-R-CA0-bgm-b-05-0-UI" /clone_lib="UI-R-CA0"

/strain="Sprague-Dawley" /db_xref="taxon:10116" /organism="Rattus norvegicus"

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REFERENCE
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                                                                                                                                          The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the
                                                                    normalized medulla library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 1-22, >AT_rich#Low_complexity
                                                                                                                                                                                                                                                   University of Iowa
451 Eckstein Medical Research Building Iowa City,
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 462)
Bonaldo, M.F., Lenno
                                  Seq primer: M13 Forward POLYA=Yes.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                        Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                                                                                             Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                Contact: Soares, MB
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; Murinae;
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KEYWORDS
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AA821607
                                                                            Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 500)
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Contact: Marra M/Mouse EST Project
                    Unpublished (1996)
                                        The WashU-HHMI Mouse EST Project
                                                            Waterston, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               library is a subtracted library derived from the following tissues: thalamus, cerebellum, hypothalamus, medulla, pons, midbrain, cerebral cortex, corpus striatum, testis, and hippocampus. For a detailed description of the library from which this clone was derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAG_TISSUE=medulla
TAG_SEQ=GAACCG"
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TAG_LIB=UI-R-CA0
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Pred. No. 3.9e-88;
Prematches 2;
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Best Local S
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                                                                     tgaggcgaaggtcctgtccagtgacatcatcagcaccaatggcgtcatccacgttataga 1754
                                                                                                                                                                                                                                          tcatgagccccggattaaagactgggatcagcagggcctcatgtcccaggttcttcgcta 1574
                                                                                                                                                                                                                                                                                                                 ccgagagcttgctggacctggcccttcaccgtgttcgcgcctttgtctagctccttcaa 1514
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GAAGGCGAAGGTTCTGTCCAGTGACATTATCAGCACCAACGGAGTCATCCACGTCATAGA
                                                                                                                                                                  tcacgtggtgggctgccagcagctgctgttggacaacctaaaagtgaccacaagtgccac 1634
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                                                                                                                                                 {\tt TCACGTGGTGGCCTG} - {\tt CAGCAGCTACTGCTGGAGAACCTAAAGGTGATCACGAGTGCCAC}
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Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; TMACE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu This clone is available royalty-
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Location/Qualifiers
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a 141 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
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/clone="IMAGE:1245316"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Soares_mammary_gland_NbMMG"
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87.9%;
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Pred. No. 1.4
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REFERENCE
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gacggtgtgaatggcactggcacgtgccagtgcgggctgggcttcaatgggacagcctgt 741
                                              AGC--CAATGTGTGAGAACCGTCATTACGAGAGAATGCTGTGCCGGCTTCTTTGGCCCCC
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plate: LLAM11559 row: j column:
High quality sequence stop: 737.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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NIH-MGC http://mgc.nci.nih.gov/.
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BI838464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               National Institutes of Health, Mammalian
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Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                               Convice Torgan: pooled pancreas and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: ECORV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 0.25. Note: this is a NIH_MGC Library."

a 182 c 224 g 157 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5222506"
/clone_lib="NNH_MGC_120"
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                FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 42 row: C column: 11
Seg primer: ATTTAGGTGACACTATAG
                                                                                                                                                               Single pass sequencing. Bases v0.980904.e. Vector identified
                                                                                                                                                                                                                                                                              Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, U
                                                                                                                                                                                                                                                                                                                                                                          Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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Fax: 402 762 4390
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Bovidae; Bovinae;
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                                                                                                                                                                                                          Email: smith@email.marc.usda.gov
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BB842118 RIKEN full-length enriched,
musculus cDNA clone F430003K15 5', mf
BB842118
Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
                                                                                                        Mammalia;
                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                      Mus musculus
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                                                                                                                                                          mouse.
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/db_xref="taxon:9913"
/clone_llb="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."
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Rodentia;
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Sciurognathi; Muridae; Murinae; Mus
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336; Conserv
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wagi, K., Fujiwake, S., Inoue, T., Gawayi, T., Tanaka, T., Watshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsu, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci.p., Shibata.y., Hayatsu.N., Sugahara.y., Shibata.K.,
M., Konno,H., Okazaki,Y., Muramatsu.M. and Hayashizaki,Y.,
Normalization and subtraction of cap-trapper-selected cDNAs i
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
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,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A.,
, Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Computer based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (200
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/clone="F430003K15"
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/strain="C57BL/6J"
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97 c 110 g
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97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. I should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC
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UI-M-BH0-aly-h-08-0-UI 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mEST@mail.nih.gov
                                                                                                             Similarity
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                                                                                                                                                                                         101
                                                                                             Conservative
                                                                                                                                                                                 /lab_host="bH108 (Life Technologies)" with a modified /note="vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_M SI library is a subtracted library derived from a mixture of normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amyddala, basal ganglia, pineal gland, striatum, hipoccampus). The driver used for subtraction consisted of a pool of 20,000 cDNA clones obtained from non-normalized and normalized libraries of these ten regions of the mouse brain."
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                                                                                                                                                                                                                                                                                                                                                                            /clone="UI-M-BH0-aiy-h-08-0-UI"
/clone_lib="NIH_BMAP_M_S1"
/dev_stage="27-32 days"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="C57BL/6J"
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82.7%;
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GACCCTCTTGGGGCACTGAGGTCCTGATGTGAGAAGECAGCCAACAGCCACAGCTACGTG 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            459 bp mRNA linear EST 01-FEB-19 yb14f01.rl Stratagene placenta (#93725) Homo sapiens cDNA clone IMAGE:71161 5' similar to similar to SP.A41735 A41735 HYALURONATE-BINDING PROTEIN TSG-6 PRECURSOR, mRNA sequence.
                                                                                                                                                                                                                                                                              High gality sequence stops: 308 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1402 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
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Insert Size: 1402
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="GDB:492058"
/db_xref="taxon:9606"
/clone="IMAGE:71161"
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                                                                                                          /organism="Homo sapiens'
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/clone_lib="Stratagene placenta

(#937225)"

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gactgacctg-tccatccgtggcaccctgttt--gtgccacagaacagtgggctaccggg 3695
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                                                                                       Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Ko,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sas,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T Muramatsu,M. and Hayashizaki,Y.
                                   Unpublished (2001)
On Jun 21, 2000 this sequence version replaced gi:8651827
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                           Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 670)
                                                                                                                                                                                                                                                                                                                                                                                                 BB086042 670 bp mRNA linear EST 18-OCT-2001 BB086042 RIKEN full-length enriched, adult male diencephalon Mus musculus cDNA clone 9330210123 3', mRNA sequence.
Laboratory for Genome Sciences Center(GSC),
                                                                                                                                                                                                                                                                                                        Mus musculus
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82.3%;
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                 Exploration Research Group,
Yokohama Institute
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Su,
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Computational Analysis of Full-Length Mouse cDNAs Compared with unman Genome Sequences Mamm. Genome. 12, 673-677 (2001) for
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs t
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Pujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Mats
%S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group Genomic Sciences Center and Genome Science Laboratory in R Division of Experimental Animal Research in Riken contribu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prepare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
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                                                                      from Lambda
BamHI"
                                                                                                                                                                                                                                                                                                                                            /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory
                                                                                                                                                                                                                              prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second
                                                                                                                                                                                                                                                                                                                                                                                                      contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                       RIKEN. Division of Experimental Animal Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="diencephalon"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diencephalon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="RIKEN full-length enriched,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="9330210123"
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                           169 c
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in Riken
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FEATURES

Query Match Best Local Similarity Matches 440; Conserv

Conservative

5.3%; 71.1%;

Score 248.6; Pred. No. 3.2e 0; Mismatches

2e-44; DB 9;

Length 670; Indels

35 ;

7;

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REFERENCE
AUTHORS
TITLE
JOURNAL
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 99a9gacagcgaccctctg9g9gcactgcggtcctgacatgagaagccagcaagcaacca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             agcgccggcaccccagagtcctcctgtgaccccttcacagaccctggagaacaggatct 4216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tgtcttggcttttggcaagcagccgcaagaatatcgcaaaccctctgtatgagacctc 4156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           caaaggcggggcttcacctcttatgttctgtattccagtacccagaagtacctgccacac 4614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ccacctcctctgagcctataccgtggttctct--cacttccatatggtgcttggtctgtt 4494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATAGTCTGAGATTGTCGTCATGGGTAAGGGGACATGTTTACAGGACACC-AGTATACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gttaatctgggattgtcgccagggctaaggagccatgttgcctggatacctgggggacct 4436
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                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
BI146461
BI146461.1 GI:
                                                                           Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can
                             found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov Plate: LLAM11148 row: g column: 15
                                                                                                                                                                                                         Mammalia; Eutheria; Rodentia; Sc
1 (bases 1 to 1066)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
                                                                                                                                                                                                                                                                         Mus musculus
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                             BI146461
602913560F1 NCI_CGAP_Li9
                                                                                                                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                            house mouse
quality sequence stop: 492
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                               GI:14606462
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                                                                                                                                                                                                                                                                                                                                                                                               1066 bp mRt Mus musculus
                                                                                                                                                                                                                                                           Craniata; Vertebrata;
Sciurognathi; Muridae
                                                                                                                                                                                                             Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                              mRNA
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cDNA clone
                                                                                                                                                                                                              Gene
                                                                                                                                                                                                                                                              Muridae;
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IMAGE:5054630 5',
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Murinae; Mus
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Best Local
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                                                                                                                                                                                                                                                                                                     CGGAA 485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gcaccgtggtgatccaaacccccaggtgctgc--catggttacttcatgccagactgtca 2474
                                                                                                                                                                                                                                                                                                                                    cggga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTTGCCTGGGAGATTTGGTCCTGACTGTCAACCCTGTGGCTGCTGTGAGCACTGCGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gctggcatgggagatttgggcctgactgtcagccccgcagctgctccgagca--tggaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acacacccatgggacagtgcctatgccacaccggcttcaacgggacagcctgcgagctct 2593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ggcctgccctggaggacca-gatacaccgtgtaacaaccggggcatgtgccgcgatctgt 2533
                                                                                                                                                                                                                                                                                                                                                                   CAGCCAACATGCTATGGACGAACAACACATGTGTGTGTAACCTTGCAATTACGAAGGTGA
                                                                                                                                                                                                                                                                                                                                                                                   tgcacgccacctgtacggagaacaacacgtgtgtgtgtaac--ttgaactacgaaggtga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       389;
                                                                                                                                                                            musculus
BB735524
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murina 1 (bases 1 to 494)
Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T. Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, F., To, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsu, Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y.,
                                                                                                                                             EST
                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                              Mus musculus
                                                                                                                             house mouse
                                                                                                                                                          вв735524.1
                                                                                                                                                                                                        вв735524
                                                                                                                                                                                                                        BB735524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5054630"
/clone=lib="NGI_CGAP_Li9"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NC
Site_2: Sall; Cloned unidirectionally. Primer: Oligo
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
72 a 330 c 276 g 188 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                        494 bp mRNA linear EST 15 RIKEN full-length enriched, 6 days neonate spleen cDNA clone F430003K15 3', mRNA sequence.
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/organism="Mus musculus"
                                                                                                                                                            GI:16134674
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                                                                              Chordata;
Rodentia;
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mismatches
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No. 1.7e-43;
                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81;
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                   tggttaatctgggattgtcgccagggctaaggagccatgttgcctggatacctgggggac
                                                                                               Email: genome res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
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RIKEN integrated sequence analysis (RISA) system--384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
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/clone="F430003K15"
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spleen"
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148 c 122 g 121 t
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Pred. No. 3.5e-43;
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Tananka,T., Matsuura
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tananka,T., Matsuura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0
Tel: 81-45-503-9222
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Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii
,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.
encyclopedia: real-time sequence clustering for construction o
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001
Please visit our web site (http://genome.gsc.riken.go.jp) for
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                          Computer-based methods for the mouse full-length cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              tcgtctgccggggcagcatctacggggagcttcccaagaacccttcgacgtcccagtact 1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gctcgcttatcaatgtctgcctaacgaacaatggcggctgcagtccattttgccttctgca 1309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGGGCCCAACCAGGCCGTCTGTAACTGCTTGCCCAAGTACACTGGAAGATGGAAAGGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cagggcccaaccaggccgtctgtaactgcttgccgaagtacactggagatggaaaggtct 1249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        324;
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 793)
                                                                                                                                              BI832486
                                                                                                                                                             mRNA sequence.
                                                                                                                                                                                  603082278F1 NIH_MGC_120
                                                                                                                                                                                                      BI832486
                                                                       Homo sapiens
                                                                                                                             BI832486.1
     NIH-MGC
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http://mgc.nci.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GRAGAGAGAGAGCTCAATTAATTAAACCCCCCCCCCC 3'].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Site_1: XhoI; Site_2: SstI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="F530009M16"
/clone_lib="RIKEN full-length
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="kidney"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/db_xref="taxon:10090"
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                                                                                                                             GI:15944036
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83.3%;
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Pred. No. 7.9e
0; Mismatches
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sapiens
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                                                                                                                                                                                  clone
                                       Hominidae;
                                                                                                                                                                                                   linear
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Вр Ş

Qγ DЪ Qy Вþ δÃ DЬ Qγ В δõ

В Ωy DЬ

LOCUS

SOURCE

Eukaryota;

Metazoa;

Chordata;

Craniata;

Vertebrata;

Euteleostomi;

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BASE CO
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                             KEYWORDS
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                                                             ACCESSION
                                                                                         DEFINITION
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JOURNAL
 ORGANISM
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                   gtagactacggatccagggccaacaagagtgaaatgtgggatgtcttctgttaccggatg 3471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cgggttgcctacccgactacgtatgcctctcagaagtgtggtgcaaacgttgttgggatc 3411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGGTTGCCTACCCCACAGCCTTCGCCTCCCAGAACTGTGGCTCTGGTGTGGGTTGGGATA 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253;
                                                                                                                                                                                            493
                                                                                                                                                                                                                        3591
                                            BB745695
BB745695.1 GI:16148634
                                                                          BB745695 474 bp mRNA
BB745695 RIKEN full-length enriched, add
cDNA_clone F530009M16 3', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc
Mus musculus
                               EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://image.llnl.gov
Plate: LLAM11556 row: 1 column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       National Institutes of Health,
              house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"Organ: pooled pancreas and spleen; Vector: pcMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:5221410"
/clone_lib="NIH_MGC_120"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 1.5e-
0; Mismatches
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                                                                                          adult male
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  Best Local Sin Matches 364;
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                              Local Similarity
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Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii
, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,
Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
Shibata, K., Shinagawa, A., Shiraki, T., Soqabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T.,
Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.,
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2001)
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Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y. and Hayashizaki,Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e mouse
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     Conservative
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                                                                                                                                                                                             prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                                                                         /note="Site_1: XhoI; Site_2: SstI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissues
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/clone="F530009M16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="kidney"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RIKEN full-length enriched, adult male kidney"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'lab_host="SOLR"
                           4.5%;
                                                                                                                                                               was cleaved with XhoI and SstI.
135 c 119 g 119 t
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     0;
Score 213.2; DB 9;
Pred. No. 1.9e-36;
D; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shibata, K., Itoh, M., Carninci, P., Sugahara
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                                                  DB 9;
                                                  Length 474;
     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIKEN Genomic
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  34;
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                                                                                                                                                                                                                                                                                                                                                                                                         cDNA was
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  7;
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T91781/c
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                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
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                                                                                                                                   source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ctgtgactctgtggtattctcctattgacgtaagcaccaaaggcggggcttcacctctta 4577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATAACTCAGA-----AGCCATACCTCACCCCTCTGGTTAGGTCTGGGGGTTGTCGTCATG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acaacactcataagccagccatacctcacccttctggtta-atctgggattgtcgccagg 4399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tgttctgtattccagtacccagaagtacctgccacacatgtgtgctcaataaatgt 4633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGTGACCCTGTGGTATCTCCTATTAACTGTAAGCACCAAAGGCAAGGCTTCATCCCATA 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tggttctct--cacttccatatggtgcttggtctgttctgccctctcttgtacccacaaa 4517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTAAGGGGACATGTTTCCAGGACACC-AGTATACCTCTGCCTCCTCTGGGCCTTCACTG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gctaaggagccatgttgcctgggatacctggggggacctccacctcctctgagcctataccg 4459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acggttccacggtga-ttcccagccccagctgtctcatggatcagttgttttaaagaatg 4340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTTCTGTATTCCAGTACCCAGAAGTACCTGCCACACGGGTGCGCTCAATAAATGT 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGCTCTCTGCACCTTCCAGATGGTGCTTGGCCTGTTCTGCCCTATCT----GTGGGTAG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACGGTTACACGGTGACTCCCCTGCTCCAGCTGTCACTTGGATCATTTGTTTTAAAGTATG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTGAGGTCCTGATGTGAGAAGCCAGCCAACAGCCACAGCCACGTGAGCCCTGAGCCATC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T91781
T91781.1
                                                                                                                                                                                                                               Insert Size: 710
High quality sequence stops: 283 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 710 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J. Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University Scho 4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 373)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T91781 373 bp mRNA linear EST 22-MAR-1999 yd52d09.sl Soares fetal liver spleen lNFLS Homo sapiens cDNA clone IMAGE:111857 3' similar to SP:2K783.1 CE00760 ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human
                                                                                                                                                                                     quality sequence stop: 283
                      /db_xref="taxon:9606"
/clone="IMAGE:111857"
                                                                                                                                                            Location/Qualifiers
  /clone_lib="Soares fetal liver spleen lNFLS"
                                                                              /db_xref="GDB:467474"
                                                                                                    /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         School of Medicine way, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST 22-MAR-1995
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BASE COUNT
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                                                                                                                                                                                                                                                                                            Matches 280;
                                                                                                                                                                                                                                                                                                    Query Match 4.3%;
Best Local Similarity 83.1%;
                                                                                                                       1290 cagtccatttgccttctgcaactacactgagcaagat 1326
                                                                               1054 tgtaaaagaacca--ccccaggaaaccgggtgtgtgtgtgtgtgcaaggcaggctataccggcg 1111
                                                                                                                                                                                                           278
                                                                                                                                                                                                                                                            995 tctgcacagccatcaatgcctgtgagaccagcaatggaggatgtt-ctacaaaggccgac 1053
                                                                                                                                                                                                                                                 338 TCTGAACAGCAATCAATTCCTTTGAGATCAGCAATGGAGGTTGCTCCTGCCAAGGCTGAC
                                         38 TAGTGAATTTGCCATCTGCAACCACGCCGAGCNCTAT 2
                                                                                                                                                                                                          TGTAAGAGAACCCACCCCCAGGAAGGCGAGTGTGCACGTGCAAAGCAGGCTACACGGGTG
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0; Mismatches 52;
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Listing first 45 summaries
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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366 KFHVIRDAKVLAVDLPTSTAWKTLQGSELSVKCGAGRDIGDLFLNGQTCRIVQRELLFDL 425

C:Species: homo sapiens (man) C:Species: homo sapiens (man) C:C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000 C:C:C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000 C:C:C:C:C:C:C:C:C:C:C:C:C:C:C:C:C:C:
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472

214

180 352

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A; Molecule type: mRNA
A; Residues: 1-2871 < YIN>
A; Cross references: GB:L29454; NID:g575509; PIDN
C:Genetics:
A; Gene: Fbn-1
C; Superfamily: unassigned EGF-related proteins;
F; 1201-1236/Domain: EGF homology < EGF>
                                                                                                                                                                                                            RESULT 2
A55624
A55624
fibrillin-1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 11-Jan-2000
C;Accession: A55624
R;Yin, W.; Smiley, E.; Germiller, J.; Sanguineti, C.; Lawton, T.; Pereira, J.
J. Biol. Chem. 270, 1798-1806, 1995
A;Title: Primary structure and developmental expression of Fbn-1, the mouse A; Reference number: A55624; MUID:95130561
A;Accession: A55624
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tive 130;
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 Score 510; DB 2;
Pred. No. 3.7e-23;
0; Mismatches 416
                                                                                                                                                PIDN: AAA56840.1;
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                                                                                                                                                                                                                                                                              IAGRHRMDACCCSVGAAWGTEECEECPLRNSREYEELCPRGPGFA----TKDITNGKPFF
                                                                                                                                                                                                                                                                                                                                                                            ISTNGVI----HVIDKLLSPKNLLITPKDALGRVLQNLTTVAANHGYTKFSKLIQDSGLLS
                                                                                                                                                                                                                                                                                                                                                                                                          INGATLKSECCSSLGAAWGSPCTICQLDPICGKGFSRIKGTQCEDI----NECEVFPG--
                                                                                                                                                                                                                                                                                                                                                                                                                                          TSATTLQ --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAVRELAGPGPFTVFAPLSSSFNHEPRIKDWDQQGLMSQVLRYHVVGCQQLLLD-NLKVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NGVCKNSPGSF - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGGC--SPFAFCNYTEQDQRICTCKPDYTGD--GIVCRGSIYGELPKNPSTSQYFFQLQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQNSAEYQALCSSGPGMTSAGTDINECALDPDICPNGICENLRGTYKCICNSGYEVDITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGLAVGLDGRWCVDTHMRSSCYGGYRRGQCVKPLFGAVTKSECCCASTEYAFGEPCQPCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----INEDGSFKCICKPGFQLASDGRYCKDINECETPGICMNGRCVNTDGSYRCECF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTSANCLLDPDGKASCKCAAGFR--GNGTVCTAINACET----SNGGC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDECLQNGRICNNGRCIN---TDGSFHCVCNAGFHVSSEGKNCEDMDECRTPNMCPNGMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIHCDQ-ACSCVHGRCSQGPLGDGS--CDCDVGW----RGVKC-DM-EITTDN-C-NGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RCECNKGFQLDIRGECIDVDECEKNPCTGGECINNQGSYTCHCRAGYQSTL--TRTECRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QPVPPGYPPGPVIPVPRPPPEYLYPSREPPRVLPVNVTDYCQLVRYLCQNGRCIPTPGSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITKMQCCCDLGRCWSPGVTVAPEMCPIRSTEDFNKLCSVPLVIPGRPEYPPPPIGPLPPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STIPGVCDGGECTNTVSSYFCKCPPGFYTSPDGTRCVDVRPGYCYTALANGRCSNQLPQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATDKGVIHGLEKVLEIQKNRC------DNNDTIIVR-GEC-----GKCSQQAP--
                                                  ---YTPMG---
                                                                                -DIDECQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·CPL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -KRTTPGNRV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -EVKMCALGTASVWDGVNGTG--TCQCGLGFNGTACETCTEGKY
                                                                                                                                                                                                                                                                                                                                                                                                                                            -GEPVSI--
                                                                                RDPLLCRGGICHNTEGTYRCECPPGHQLSP--NISACIDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -ICECSPESTLDPTKTICIETIKGT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RSVFIGCQPQCVRTI-ITRACWLAS-LAHNAK--PAPG---
                                                  -QCLCHTGFNGT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -ETKPLRET----RKCIYSIYFMGK-------
                                                                                                                                                --GQCVNTPGDFECKCD-EGYESGFMMKNCM-
                                                                                                                                                                                                                                                                                                          -KALEALPPEQQDFLFNQDNKDKLKSYLKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -STKADC--
                                                                                                              -CQACPGGPDTPCNNRGMCRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                        -SVSQDTVFINNEAKVLSSDI
                                                                                                                                                                                                                                                                                                                                              ---ETCFLKYDDEECTLP
                                                -----ACE-LCWH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CWQTVIDGRCEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CVCKAGYTGD - - G
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1156

1112

1026 737

677 970 631 574

865

919

541

482

817 426 760 372 700 640 346 587 304 530 255

352

852

2000 L.Y.	ESULT 4 47221 47221 ibrillin 1 precursor - human (fragment) ;Species: Homo sapiens (man) ;Date: 02-Jun-1995 #sequence_revision 25-Apr-1997 #text_change 21-Jul- ;Accession: A47221; 154355; S17064; 159574; S17062; S62111; A34198 ;Corson, G.M.; Chalberg, S.C.; Dietz, H.C.; Charbonneau, N.L.; Sakai, enomics 17, 476-484, 1993	RE RE C;
587	1552PDFQLNATGVGCVDNRVGNCYLKFGPRGDGSLSCN 1	da
.176	TTYASQKCGANVVGIVDYGSRANKSEMWDVFCYRMKDVNCTCKAGYVGDG-FSCS 1	Qy
1551	1503 PGMEHCICDDG-YELDRTGGNCTDIDECADPINCVNGLCVNTPGRYE-CNC	дь
1118	VFHLRSPLGQYKLTFDKAKEACAKEAATIATYNQLSYAQKAKYHLCSAGWLESGR	Qy
1502	GQCLNVPGAYRCECEMGFTPASDSRSCQDIDECSFQNICVFGTCNNL	ДĎ
1062	RCHPDASCADLYFQ	Qy
1442	1389 REGWYGNGIKCIDLDECANGTH-QCSINAQCVNT-PGSYRCACSEGFTGDGFTCSD	Db
1035	KGYKGDGYSCIEIDPCADGVNGGCHEHATCRMTGPGKHKCECKSHYVGDGVDCEPEQLP	Qy
1388	1330 MFGEC-ENTKGSFICHCQLGYSVKKGTTGCTDVDECEIGAHNCDMHASCLNVPGSFKCSC	Db
975	922 VHATCTENNTCVCNLNYE-GDGTT-CTVVDFCKQNNGGCAKVAKCSQKGTQVSCSC	Оу
1329	1280 CENNPDIC-DGGQC-TNIPGEYR	DЬ
921	OCDEGITGSGECLCETG	Qy
1279	1227 TPDRQGCTDIDECMIMNG	Дb
864	DCQACPGGPDTPCNNRGMCRDLYTPMGQCLCHTGFNGTACEL	Qy
1226	1176 CDCPLGHELSPSREDCVDINECSLSDNLCRNGKCVNMIGTYQCSCNPG	ρb
820	REKGVKKKCI-YNPLPERRNVEGCQN-LCTVVIQTPRC-CH-GY-F	Qy
1175	1120 GSGICVNTPGSFECECFEGYESGFMMMKNCMDIDECERNPLLCF	DЬ
765	GIDCLLMNPTLGGRC-DTFTTFDIPGE	Qγ
1119	1065 KDINECKAFPGMCTYGKCRNTIGSFKCRCNNGFALDMEERNCT	da
727	QGSELSVRCGTGSDIGELFLNEQMCRFI	Qy
1064	1009 VPGKERMDACCCAVGAAWGTECEECPKPGTKEYETLCPRGPGFANRGDILTGRPFC	рb
677	SIHTPVTVFWPTDKALEALPPEQQDFLFNQDNKDKLKSYLKF-	Qy
1008	962 GRCVNSKGSFHCECPEGLTLDGTGRVCLDIRMEHCFLKWDEDECIHP	ф
631	TNGVIHVIDKLLSPKNLLITPKDALGRVLQNLTTVAANHGYTKFSKLIQDSGLLS	Оy
961	925CERCELDAACPRGFARIKGVTCEDVNECEVFPGVCPN	Db
571	QLLLDNLKVTTSATTLQGEPVSISVSQDTVFINNEAKVLS	Qy
924	892 WLNIQDNRCEVNINGATLKSECCATLGGA	Db
516	PKNPSTSQYFFQLQEHAVRELAGPGPFTVFAPLSSSFNHEPRIKDWDQQ	Qy
891	839 ETETCEDVNECESNPCVNGACRNNLGSFHCECSPGSKLSSTGLICIDSLKGTC	Db
465	NVCLTNNGGCSPFAFCNYTEQDQRICTCKPDYTGDGIVCRGSIYG	Qy
838	781 RGTYRCNCNSGYEPDASGRNCIDIDECLVNRLLCD-NGLCRNT-PGSYSCTCPPGYVLPT	Db
412	364CKAGYTGDGIVCLEINPCLENHGGCDRNAECTQTGPNQAVCNCLPKYTG	Qy

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A.Cross-references: EMBL.X63556
R.Dietz, H.C.; Valle, D.; Francomano, C.A.; Kendzior, R.J.
Science 259, 680-683, 1993
A.; Title: The skipping of constitutive exons in vivo induced by nonsense mutations.
A.; Reference number: I59574; MUID:93157831
A.; Accession: I59574; MUID:93157831
A.; Accession: I59574
A.; Status: preliminary; translated from GB/EMBL/DDBJ
A.; Molecule type: DNA
A.; Residues: 2217-2288, 71, 2290-2325 < RES>
A.; Residues: 2217-2288, 71, 2290-2325 < RES>
A.; Residues: 3217-2288, 71, 2290-2325 < RES>
A.; Godfrey, M.; Vitale, E.; Hori, H.; Mattel, M.G.; Sarfarazi, M.; Tsipouras, Nature 352, 330-334, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Introns: 2236/1; 2258/1; 2297/1
C;Superfamily: unassigned EGF related proteins; EGF homology
C;Superfamily: unassigned EGF-related proteins; EGF homology
C;Keywoods: alternative splicing; calcium binding; extracellular matrix; glycoprotein
F;1-3002/Product: fibrillin (5'-region exon A splice form) (fragment) #status predict
F;132-3002/Product: fibrillin (5'-region exon C splice form) #status predicted <MATC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 1166-1176, 'X',1178-1180,'D',1182-1185 <LEE2>
R; Maddox, B.K.; Sakai, L.Y.; Keene, D.R.; Glanville, R.W.
J. Biol. Chem. 264, 21381-21385, 1989
A; Title: Connective tissue microfibrils. Isolation and characterization of three large A; Reference number: A34198; MUID:90078246
A; Reference number: A34198; MUID:90078246
A; Recession: A34198
A; Accession: A34198
A; Microfibrilin is a major component of elastin-associated microfibrils.
C; Comment: Fibrillin is a major component of elastin-associated microfibrils.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:L13923; NID:g306745; PIDN:AAB02036.1; PID:g306746 R;Maslen, C.L.; Corson, G.M.; Maddox, B.K.; Glanville, R.W.; Sakai, L.Y. Nature 352, 334-337, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 132-3002 <PER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-337, "T',339-1029 <COR>
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A;Cross-references: GB:X63556
A;Cross-references: GB:X63556
R;Pereira, L.V.; D'Alessio, M.; Ramirez, F.; Lynch, J.; Sykes, B.; Pangilinan, T.; Bo
Hum. Mol. Genet. 2, 961-968, 1993
A;Tille: Genomic organization of the sequence coding for fibrillin, the defective gen
A;Reference number: I54355; MUID:93372860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Fibrillin binds calcium and is coded by cDNAs that reveal a multidomain stru A;Reference number: A47221; MUID:94010947 A;Accession: A47221
                                                                                                             Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 'VLYTVPTFLSYNKML',944-1444 <LEE1>
A;Cross-references: EMBL:X62008; NID:g31398; PIDN:CAB56534.1; PID:g5924015
A;Accession: S62111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Linkage of Marfan syndrome and a phenotypically related disorder to two diff A;Reference number: S17062; MUID:91304567 A;Accession: S17062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1030-3002 <MAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Partial sequence of a candidate gene for the Marfan syndrome. A;Reference number: S17064; MUID:91304568
A;Accession: S17064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A; Accession: I54355
                                          Дb
                                                                                                                                                                                                                                                                                                                                                                                                                        F;1332-1367/Domain:
F;1457-1492/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: GDB: FBN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Genetics:
                                                                                                                                                                                      Query Match
Best Local S
Matches 261
                                                                                                                    189 PQCVRTIITRACWLAS-LAHNAK--PAPG------EVKMCALGTASV 226
                                                                                                                                                                                                                                 Local Similarity
                                          PRVLPVNVTDYCQLVRYLCQNGRCIPTPGSYRCECNKGFQLDLRGECIDVDECEKNPCAG 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15q21.1-15q21
                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                      EGF homology <EGF2>
EGF homology <EGF1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDB:127115; OMIM:134797; OMIM:154700
                                                                                                                                                                               6.3%; Score 497.5; DB 2;
21.7%; Pred. No. 2.3e-22;
                                                                                                                                                                                                                                                                Length 3002;
                                                                                                                                                                                          Indels 465;
                                                                                                                                                                                   Gaps
                                                                                                                                                                                              70;
2
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ictu	QY 227	7 WDGVNGTGTCQCGLGFNGTACETCTEGKYGIHCDQ-ACSCVHGRCSQGPLGDGSCD 281
	Db 633	GECINNOGS
	Оу 282	CDVGWRGVKCDMEITTDNCNGTCHTSANCLLDPDGKASCKCAAGERG
nao	DD 688	CNAGEHVI KUGKNCE-
e T	Оу 329	9 NGTVCTAINACETSNGGC 346
	Db 738	B DGRYCKDINECETPGICMNGRCVNTDGSYRCECFPGLAVGLDGRVCVDTHMRSTCYGGYK 797
	Оу 347	7
	Db 798	8 RGQCIKPLFGAVTKSECCCASTEYAFGEPCQPCPAQNSAEYQALCSSGPGMTSAGSDINE 857
	Qy 362	
	Db 858	8 CALDPDICPNGICENLRGTYKCICNSGYEVDSTGKNCVDINECVLNSLLCD-NGQCRNT- 915
	QY 399	
	Db 916	6 PGSFVCTC-PKGFIYKPDLKTCEDIDECESSPCINGVCKNSPGSFICECSS 965
	Qy 451	DYTGDGIVCRGSIYGELPKNPSTSQYFFQLQEHAVRELAGPGPFTVFAPLSSSFNHEP 508
	pb 966	6 ESTLDPTKTICIETIKGT 983
	Qy 509	9 RIKDWDQQGLMSQVLRYHVVGCQQLLLD-NLKYTTSATTLQGEPVSISV 556
	Db 984	4CWQTVIDGRCEININGATLKSQCCSSLGAAWGSPCTL-C 1021
70	Qy 557	
ere	Db 1022	2 QVDPICGKGYSRIKGTQCEDIDECEVFPGVCKNGLCVNTRGSFKCQCPSGMTL 1074
	0у 599	DALGRVLQNLTTVAANHGYTKFSKLIQDSGLLSVITDSIHTPVTVFWPTDKA 650
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	Qy 651	1LEALPPEQQDFLFNQDNKDKLKSYLKFHVIRDSKALASDLPRSASWKTLQGSEL 704
	Db 1129	9 MRNTPEYEELCPRGPGFATKEITNGKPFFKDINECKMIPSLCTHGKCRNTIGSF 1182
ī 1	ОУ 705	
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	Qy 741	
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	Qу 783	
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; z	Qy 821	
ed	Db 1360	0 LMPDQRSCTDIDECEDNPNICDG-GQCTNIPGEYRCLCYDGEMASE 1404
	Оу 872	PD
	Db 1405	5DMKTCVDVNECDLNPNICLSGTCENTKGSFICHCDMGYSGKKGKTGCTDINECEIGA 1461
	Оу 918	
_	Db 1462	2 HNCGKHAVCTNTAGSFKCSCSPGWIGDGIKCTDLDECSNGTHMCSQHADCKNTMGSYR 1519
	Qу 973	CSCKKGYKGDGYSCIEIDPCADGVNGGCHEHATC
	Db 1520	0 CLCKEGYTGDGFTCTDLDECSENLNLCGNGQCLNAPGGYRCECDMGFVPSADG 1572
_	ОУ 1027	7 VDCEPEQLPLDRCLQDNGQCHPDASCADLYFQDTTVGVFHLRSPLGQYKLTFDKAK 1082

535	8 NGVIHVIDKLLSPKNLLITPKDALGRVLQNLTTVAANHGYTKFSKLIQDSGLLSVITD 6	Qy 571	
563	7GCAQ-LCKNRKGSRRCQCFAGY-ILAHDEKSCVAASDSADIFSNDIEDY 5	Db 517	
577	8 LMSQVLRYHVVGCQQLLLDNLKVTTSATTLQGEPVSISVSQDTVFINNEAKVLSSDIIST	Qy 511	
516	C	Db 505	
517	9 CRGSIYGELPKNPSTSQYFFQLQEHAVRE-LAGPGPFTVFAPLSSSFNHEPRIKDWDQQG	Qy 45	
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347	-ITTDNCNGTCHTSANCLLDPDGKASCKCAAGFRGNGTVC-TAINACETSNGGCS:	Qy 295 Db 280	
294	NGTACETCTEGKYGIHCDQACSCVHGRCSQGPLGDGSCDCDVGWRGVKCDME	Oy 243 Db 231	
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228 170	SVFIGCQPQCVRTIITRACWLASLAHNAKPAPGEVKMCALGTASVWD	Qy 182 Db 125	
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0 ± 0 ± 0 ± 0	clone Y64G10A	A; Experi	
V64610A F	NRI.AT.110498: NTD-61540303: DTDN-CAR54471 1: CESD.	A;Residu	
	ion: T27283 : preliminary; translated from GB/EMBL/DDBJ	A; Access A; Status	
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1999	protein Y64G10A.f - Caenorhabditis elegans Taenorhabditis elegans Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-	T27283 hypothetical C;Species: C C;Date: 15-C C;Accession: B:Ainscough	
	4 GNC 161	161	
	3 FAC 1085	108	
1613		Db 1573	

RESULT A54105 fibrill C;Speci C;Acces R;Zhang J;Title A;Refer A;Acces A;Molec	Db	Qу	Db	Qy	Db	QУ	Db	Qy	Db	Qy	Db	Qy	Ф	Qy	Db	Qy	Db	Qy	Db	Qу	Db	Qy	Db	Qy	da	Qy	Db	Qy	Db
cusse:	1287	1171	1254	1111	1211	1051	1151	1016	1091	997	1039	943	985	895	928	849	868	848	808	826	755	792	701	754	647	696	617	636	564
in-2 precursor - human ses: Homo sapilens (man) 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 17-Nov-2000 19-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 17-Nov-2000 sion: A54105; S17063; S31101 H.; Apfelroth, S.D.; Hu, W.; Davis, E.C.; Sanguineti, C.; Bonadio, J.; Mecha Biol. 124, 855-863, 1994 Structure and expression of fibrillin-2, a novel microfibrillar component pr ence number: A54105; MUID:94165150 sion: A54105 si preliminary; nucleic acid sequence not shown; not compared with conceptual sle type: mRNA	DPISCHCS 1294	DGFSCS 1176	PGW-SGEHCEKSCVSG-HYGAKCEETCECENGALC 1286	AGWLESGRVAYPTTYASQKCGANVVGIVDYGSRANKSEMWDVFCYRMKDVNCTCKAGYVG 1170	ECIDGWTGPSLCPFGQFGRNCAQRCNCKNGASCDRKTGRCECL 1253	SCADLYFQDTTVGVFHLRSPLGQYKLTFDKAKEACAKEAATTATYNQLSYAQKAKYHLCS 1110	SCQCSNGASCDRVTGFCDCPSGFMGKNCESECPEGLWGSNCMKHCLCMHGGECNKENGDC 1210	DNGQCHPDA 1050	NAICDCTTUDTSMYNPFVARO		CDETCDSGLFGAGCKGICSCQNGATCDSVTGSCECRPGWRGKKCDRPCPDGR 1090	ITCTVVDFCKQNNGGCAKVAKCSQKGTQVSCSCKKGYKGDGYSCIEIDPCADGV 996		CLCETGWTAASCDTPTAVFAVCTPACSVHATCTENNTCVCNLNYEGDG 942	SCVNGAKCDESDGSCHCTPGFYGATCSEVCPTGFFGIDCMQLCKCQNGAICDTSNGS 984	GQCLCHTGFNGTAC-ELCWHGRFGPDC-QPRSCSEHGQCDEGITGSGE 894	HKSKVCHHVTGTCTCLPGKTGPLCDQCLIFVETIEFDIAFSINVIACAPNTYGPNCAHTC 927	M 848	: : : :	ACPGG	PCPHETFGKNCRFPCKCARENSEGCDEITGKCRCKPGYYGHHCKRMCSPGLFG 807	TVVIQTP	CEDPEKCSDGPCPDGFYGSQCNLKCRNDCPNGRCDPVFGYCTCPDGLYGQSCEK 754	TFTTFDIPGECGSCIFTP	KCSMRGSGLLSKCDCPSGYTGEKCBQTCRNGYWGVDCAHKCSCKLCDPSTGSCR 700	LNEOMCREIHRGLLFD	EVRTDPSEKCPNGFFGSTCQLSCSDCQNGG 646	SIHTPVTVFWPTDKALEALPPEQQDFLFNQDNKDKLKSYLKFHVIRDSKALASDLPRSAS 695	SKVPGLDSIDEVISSIESYPADESPRPLVFGRRRHVKACVNFQGTLSLELFSS 616

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 752-1407,'R',1409-1489,1791,'GS',1794-1796,'QLI',1922-1923,'LD',1926,'P',
A;Cross-references: EMBL:X62009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, A; Reference number: S31101 A; Accession: S31101
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A; Residues: 752-1489,1791,'GS',1794-1796,'QLI',1922-1923,'LD',1926,'P',1928
A; Cross-references: EMBL:X62009
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A; Cross-references: GB: U03272
A; Cross-references: GM: Vitale,
Nature 352, 330-334, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 290;
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Best Local (
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                                                                                                                                                                                                                                                                                                                                             CCCANPDYGFGEPCQPCPAKNSAEFHGLCSSGVGITVDGRDINECALDPDICANGICENL
                                                                                                                                                                                                                                                                                                                                                                                                                                                GGC----STKADCKRTTPG-----NRVCV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D--NC--NGTCHTSANCL----LDPDGKASCKCAAGF--RGNGTVCTAINACET----SN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T----ACETCTEGKYGIHCDQ-ACSCVHGRCSQGPLGDGS--CDCDVGWRGVKCDMEITT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RCIPTVSSYRC-ECNMGYK-QDANGDCIDVDECTSNPCTNGDCVNTPGSYYCKCHAGFQR
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                               VIDKLLSPKNLLITPKDALGRVLQNLTTVAANHGYTKFSKLIQDSGLLSV----ITDSIH
                                                                                                                                     WLNIQDSRCEVNINGATLKS-----ECCATLGAA-----
                                                                                                                                                                                                        ETETCEDINECESNPCVNGACR-----NNLGSFNCECSPGSKLSSTGLICIDSLKGTC
                                                                                                                                                                                                                                                                                                                                                                                                                GHCINSEGSFRCDC---PPGLAVGMDGRVCVDTHMRSTCYGGIKKGVCVRPFPGAVTKSE
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----CECPEGLTL---DGTGRVCLD---IRMEQCYLKWD---EDECIHPVPGKFRMDACC
                                                                 --CERCELDT-ACPRGLARIKG----
                                                                                                 VGCQQLLLDNLKVTTSATTLQGEPVSISVSQDTVFINNEAKVL - - - - - SSDIISTNGVIH
                                                                                                                                                                     PKNPSTSQYFFQLQEHAVRELAGPGPFTVFAPLSSSFNHEPRIKDWDQQGLMSQVLRYHV
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                                                               -VTCEDV---NECEVFPGVCPNGRCVNSKGSFH
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nes 400;
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CAVGAAWGTECEECPKPGTKEYETLCPRGAGFANRGDVLTGRPFYKDINECKAFPGM 1082
LPRSASWKTLQGSELSVRCGTGSDIGELFLNEQMCRFIHRGLLFDVGVAY 739
CTYGKCRNTIGSFKCRCNSGFALDMEERNCTDIDECRISPDLCGSGICVNTPGSF 1137
GIDCLLM
ECECFEGYESGFMMKKNCMDIDGCERNPLLCRGGTCVNTEGSFQCDCPL
TVVIQTPRC-CH-GY-EMPDCQACP
GHELSPSREDCVDINECSLSDNLCRNGKCVNMIGTYQCSCNPGYQATPDRQGCTDIDE 1244
;
GGPDTPCNNRGMCRDLYTPMGQCLCHTGFNGTACELCWHGRFGPDCQP 876
CMIMNGGCDTQCTNSEGSYECSCSEGYALMPDGRSCADIDECENNP 1290
RSCSEHGQCDEGITGSGECLCETGWTAASCDTPTAVFAVCTPACSVHA 924
DIC-DGGQC-TNIPGEYRCLCYDGFMASMDMKTCIDVNECDLNSNICMFGEC
FCKQNNGGCAKVAKCSQKGTQVSCSCKK
ENTKGSFICHCQLGYSVKKGTTGCTDVDECEIGAHNCDMHASCLNIPGSFKCSCREG
SPGKHKCECKSHYVGDGVDCEPEQLPLC
WIGNGIKCIDLDECSNGTH-QCSINAQCVNT-PGSYRCACSEGFTGDGFTCSDVDE 1451
CLQDNGQCGV 1064
CAENINLCENGQCLNVPGAYRCECEMGFTPASDSRSCQDIDECSFQNICVSGTCNNLPGM
FHLRSPLGQYKLTFDKAKEACAKEAATIATYNQLSYAQKAKYHLCSAGWLESGRVAY 1121
FHCICDDG-YELDRTGGNCTDIDECADPINCVNGLCVNTPGRYE-CNC
acvamanunceckacvucna-ESCS 11
ETITIVAČINCA VATA ATI ATI ATI ATI ATI ATI ATI ATI ATI
SDS ATTY

A40043

Cell 66, 649-661, 1991
A;Title: TAN-1, the human homolog of the Drosophila
A;Reference number: A40043; MUID:91347367
A;Accession: A40043
A;Status: preliminary; nucleic acid sequence not she notch protein homolog TAN-1 precursor - human (:Species: Homo sapiens (man) (:Species: Homo sapiens (man) (:Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 13-Aug-1999 (:Accession: A40043 R:Ellisen, L.W.; Bird, J.; West, D.C.; Soreng, A.L.; Reynolds, T.C.; Smith. Notch gene, is broken by Smith, S.D.;

A; Molecule type: mRNA A; Residues: 1-2555 <ELL>

shown;

not

compared with

conceptual

A;Cross-references: GB:M73980 C;Superfamily: unassigned ankyrin repeat proteins; F;261-292/Domain: EGF homology <EGX1> F;1960-1992/Domain: F;1994-2026/Domain: F;1149-1180/Domain: F;1187-1218/Domain: F;987-1018/Domain: F;494-525/Domain: EGF homology <EGF1> F;1927-1959/Domain: F;1233-1264/Domain: 2060-2092/Domain: EGF homology <EGX2> EGF homology <EGX3>
ankyrin repeat homology
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<AN3>
<AN4> <AN5> <AN1> ankyrin repeat homology; EGF homol

9	AKCSQKGTQVSCSCKKGYKGDGYSCIEI	93 104	
8	SEHGQCDEGITGSGECLCETGWTAASCDTPTAVFAVC-TPACSVHATCTENNTCVCN 935	Qy 880 Db 993	0 0
2 0	CHTGFNGTACE	Qy 853 Db 933	D Ø
2 2	NICTVVIQTPRCCHGYFMPDCQACPGGPDTPCNNRGMCRD-LYTPMGQCL 852	Qy 804 Db 886	
0ι ω	IPGECGSCIFTPKCPLKSKPKGVKKKCIYNPLPFRRNVEGCQ 803	Qy 762 Db 833	Qу Дъ
1 2	GTGSDIGELFLNEOMCRFIHRGLLFDVGVAYGIDCLLMNPTLGGRCDTFTTFD 761	Qy 709 Db 779	dd Qy
ш ш	QDFLFNQDNKDKLKSYLKFHVIRDSKALASDLPRSASWKTLQGSELSVRC 708 :	Qy 659 Db 726	g V
01 &	DALGRVLQNLTTVAANHGYTKFSKLIODSGLLSVITDSIHTPVTVFWPTDKALEALPPEQ 658	Qy 599 Db 694	d Qy
ω φ	KVTTSATTLQGEPVSISVSQDTVFINNEAKVLSSDIISTNGVIHVIDKLLSPKNLLITPK 598	Qy 539 Db 652	0 0
1 8	AVRELAGPGPFTVFAPLSSSFNHEPRIKDWDQQGLMSQVLRYHVVGCQQLLLDNL 538	Qy 484 Db 623	0 0
ς ω	GGCSPFAFCNYTEQDQRICTCKPDYTGDGIVCRGSIYGELPKNPSTSQYFFQLQEH 483	Qy 428 Db 567	D O
5 7	YTGDGIVCLEINPCLENHGGCDRNAECTQTGPNQAVCNCLPKYTGDGKVCSLINVCLTNN 427	Qy 368 Db 520	D Ø
9 7	PDGKASCKCAAGFRGNGTVCTAINACETSNGGCSTKADCKRTTPGNRVCVCKAG 367	Qy 314 Db 470	0 0
ψω	YGIHCDQACSCVHGRCSQGPLGDGSCDCDVGWRGVKCDMEITTDNC-NGTCHTSANCLLD 313	Qy 255 Db 420	0 0
4 6	-PAPGEVKMCALGTASVWDGVNGTGTCQCGLGFNGTACETCTEGK 254	Oy 211 Db 361	0 0
0	KCIYSIYFMGKRSVFIGCQPQCVRTIITRACWLASLAHNAK 210	Qy 170 Db 310	0 0
9 9	EKVLEIQKNRCDNNDTIIVRGECGKCSQQAPCPLETKPLRETR 169 : : : : : :	Qy 127 Db 256	
74;	Query Match 6.3%; Score 492; DB 2; Length 2555; Best Local Similarity 21.7%; Pred. No. 4.2e-22; Matches 269; Conservative 120; Mismatches 445; Indels 406; Gaps	Query M Best Lo Matches	

Qy 990 Db 1104	DPCADGVNGGCHEHATCRWTGPGKHKCECKSHYVGDGVD-CEPEQL/PLDRCLQD 1042
Qy 1043 Db 1152	NGQCHPDASCADLYFQDTTVGVFHLRSPLGQYKLTFDKAKEACAKEAATIATYNQLSYAQ 1102
	AKYHLCSAGWLESGRVAYPTTYASQKCGANVVGIVDYGSRANKSEMW 1
Qy 1151 Db 1238	DVFCYRMKDVNCTCKAGYVGDGESCSGNLLQVL 1183
RESULT 8 A35844 Xotch prot C; Species: C; Date: 12 C; Accessic R; Coffman, Science 24 A; Title: 24	ican clawed frog laevis (African claw #sequence_revision is, W.; Kintner, C. 441, 1990
A;Title: A;Referen A;Accessi A;Status: A;Molecul	osophila nce not s
A; Restlate; C; Superfai C; Keyword: E; 146-177 E; 184-215 F; 222-254 F; 456-487 F; 456-487	A; restoues: 1-2024 <-CUF'> C; Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol C; Keywords: transmembrane protein F;146-177/Domain: EGF homology <-EGX1> F;184-215/Domain: EGF homology <-EGF1> F;222-254/Domain: EGF homology <-EGF2> F;456-487/Domain: EGF homology <-EGF2> F;757-788/DOmain: EGF homology <-EGFX2>
F;1924-19 F;1957-19 F;1991-20 F;2024-20 F;2057-20	16/Domain: ankyrin repeat homology <an1> 19/Domain: ankyrin repeat homology <an2> 19/Domain: ankyrin repeat homology <an3> 10/Domain: ankyrin repeat homology <an3> 16/Domain: ankyrin repeat homology <an4> 19/Domain: ankyrin repeat homology <an5></an5></an4></an3></an3></an2></an1>
Query Match Best Local S Matches 297	y Match Local Similarity 21.7%; Pred. No. 8.5e-22; hes 297; Conservative 135; Mismatches 463; Indels 476; Gaps 91;
Оу 105 Db 86	YVNEAPINYT
Oy 151 Db 139	KCSQQAPCPLETKPLRETRKCI-YSIYFMGKRSVFIGCOP
Oy 190 Db 191	QCVRTIITRACWLASLAHNAKPAPGEVKMCALGTASVWDGVNGTGTCQ 237
Qy 238 Db 235	CGLGFNGTACETCTEGKYGIHCDQAC 263
Qy 264 Db 295	SCYHGRCSQGPLGDGSCDCDVGWRGVKCDMEITTDNC-NGTCHTSANCLL 312
Qy 313 Db 351	DPDGKASCKCAAGFRGNGTVCTAINACETSNGGCSTKADCKRTTPGNRVCVCKAGY 368

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                                                                                                                                                                                                                                                                                                    GTCQDSYGTYKCTCPQGY--TGLNCQNLVRWC--DSSPCKNGGKCWQTNNFYRCECKSGW
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                             NKSEMWDVF-----CY-----RMKDVNCTCKAGYVGDGFSCSGNLLQVL 1183
                                                                                                              ATYNQLSYAQKAK---YHLCSAG-----WLESGRVAYPTTYASQKCGANVVGIVDYGSRA
                                                                                                                                                 ---VDEC--SPNPCQNGATCTDY-----
                                                                                                                                                                                   QLPLDRCLQDNGQCHPDASCADLYFQDTTVGVFHLRSPLGQYKLTFDKAKEACAKEAATI
                                                                                                                                                                                                                        TGVYCDVPSVSC-EVAAKQQGVDIVHLCRNSGMCVDTG-NTHFCRCQAGYTGS--YCEEQ
                                                                                                                                                                                                                                               KG-----DGYSCIEIDPCADGVN--GGCHEHATCRMTGPGKHKCECKSHYVGDGVDCEPE
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                                                                                                                                                                                                                                                                                                                                                                                                              LCWHGRFGPDCQPRSCSEHGQCDEGITGSGECLCETGWTAASCDTPTAVFAVCTPACSVH
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                                                                         {\tt AGYHGVNCSEEINECLSHPCQNGGTCIDLINTYKCSCPRGTQGVHCEINVDDCTPF-}
YDSFTLEPKCFNNGKCIDRYGGYNCICPPGFYGE--RCEGDVNECL 1272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPTDKALEALPPEQQDFLFNQDNKDKLKSYLKFHVIRDSKALASDLPRSASWK
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RESULT A24420

9

notch

protein

fruit

fly

(Drosophila

melanogaster)

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A;Gene: notch, opu
A;Gross-references: FlyBase:FBgn0004647
A;Map position: 8.96-9.36
A;Introns: 53/3; 84/3; 171/3; 240/3; 283/3; 2333/3; 2436/3;
A;Introns: 53/3; 84/3; 171/3; 240/3; 283/3; 2333/3; 2436/3;
A;Introns: 53/3; 84/3; 171/3; 240/3; 283/3; 2333/3; 2436/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 17, 6463-6471, 1989
A; Title: Hypervariability of simple sequences as a A; Reference number: S09358; MUID:89385974
A; Accession: S09358
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A;Nolecule type: DNA
A;Residues: 1-2703 <KID>
A;Residues: 1-2703 <KID>
A;Cross_references: GB:K03508; NID:g157991; PIDN:AAA28725.1; PID:g157993
A;Cross_references: GB:KIM:; Xu, T.; Artavanis-Tsakonas, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Kidd, S.; Kelley, M.R.; Young, M.W. Mol. Cell. Blol. 6, 3094-3108, 1986 A;Reference number: A24420; MUID:8706 A;Accession: A24420
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F;2538-2568/Region: glutamine-rich
F;2538-2568/Domain: neurogenic repetitive el
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A; Accession: A24768
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C;Accession: A24420; A24768; S09358; A05267
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F;1746-1762/Domain:
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A; Residues: 2504-2576, 'E', 2578-2611 <WHA2>
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NCSQGF - TGPRCETNINECESH - PCQNEGSC - LDDPGTFRCVCMPGFTGTQCEIDIDE 529
                                          KCAAGFRGNGTVC-TAINACETSNGGCSTKADCKRTTPGNRVCVCKAGYTG----
                                                                                     CHADAICDTSPINGSYACSCATGYKGVDCSEDI--DECDQGSPCEHNGICVNTP-GSYRC
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                                                                                                                                                                               ICVNGWAGL-DCSNNTDDCKQAACEYGATCIDGVGSFYCQCTKGKTGLLCHLDDACTSNP 417
                                                                                                                                                                                                                         MCALGTASVWDGVNGTGTCQCGLGFNGTACE-----TCTEGKYGI--HCDQACS---
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                                                                                                                                                                                                                                                                                                                                                                                             DGINGY-NCSCLAGYSGANCQYK---LNKCDSNPCLNGATCHEQNNEYTCHCPSGFTGK-
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                                                                                                                                                    CQNGGTCHDRV----MNFSCSCPPGTMGII----CEINKDDCKPGACHNNGSCIDRVGGFE
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C;Date: 20-Feb-1995 #sequence_revision 20-Feb-C;Accession: A55567 R;Tilstra, D.J.; Li, L.; Potter, K.A.; Womack, Genomics 23, 480-485, 1994 A;Title: Sequence of the coding region of the A;Reference number: A55567; MUID:95137597 A;Accession: A55567 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-2871 <TIL> A;Cross references: GBIL> A;Cross references: GBIL28748; NID:9508427; PIC;Superfamily: unassigned EGF-related proteins F;1201-1236/Domain: EGF homology <EGF>
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                                                    AW--NKPCEQCP
                                                                                     FWPTDKALEALPPEQQDFLFNQDNKDKLKSYLKFHVIRDSKALASDLPRSASWKTLQGSE
                                                                                                                        MRRSLCYRNYYADNQTCDGELLFNMTKKMCCCSYN---
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-LSVRCGTGSDIGELFLNEQMCRFIHRGLLFDVGVAYGIDCLLMNPTLGGRCDTFT:: | | | | |
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Pred. No. 2.4e-21;
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	164 PLRETRKCIYSIYFMGKRSVFIGCQPQCVRTIITRACWLASLAHN : ::
NDTIIVRGECGKCSQQAPCPLETK 163 	QY 115 NVATDKGVIHGLEKVLEIQKNRCDNNDTIIVRGECGK 1
Length 1111; Indels 441; Gaps 70;	Query Match 6.1%; Score 480.5; DB 2; Ler Best Local Similarity 22.2%; Pred. No. 7.9e-22; Matches 251; Conservative 98; Mismatches 341; Inc
947/2; 1017/1; 1083/1 repeat homology; EGF homology	Genetics: Gene: CESP:Y47H9C.4 Map position: 1 Introns: 50/2; 84/2; 150/1; 238/3; 342/3; 797/1; 851/1; Superfamily: unassigned ankyrin repeat proteins; ankyri
:GN00019; CESP:Y47H9C.4	Molecule type: DNA Molecule type: DNA Residues: 1-1111 <wil> Cross-references: EMBL:AL032657; PIDN:CAA21739.1; GSPDB Experimental source: clone Y47H9C</wil>
	R;Harris, B. submitted to the EMBL Data Library, October 1998 A;Reference number: 220293 A;Accession: T26972 A;Accession: Tminary: translated from GB/EMBL/DDBJ A:Status: preliminary: translated from GB/EMBL/DDBJ
_change 17-Mar-2000	RESULT 11 T26972 T26972 Rypothetical protein Y47H9C.4 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_C C; Accession: T26972
	Qy 1167 GYVGDGFSC 1175 : Db 2156 GYILQGNEC 2164
CYRMKDVNCTCKA 1166	Qy 1137IVDYGSRANKSEMMDVFCYRMKDVN-
ANVVG 1136 : CALKGEGWGDPC 2096	QY 1086 AKEAATIATYNQLSYAQKAKYHLCSAGWLESGRVAYPTTYASQKCGANVVG
YKLTFDKAKEAC 1085 : FSLSSTGRRC 2053	QY 1026 GVDCEPEQLPLDRCLQDNGQCHPDASCADLYFQDTTVGVFHLRSPLGQYKLTFDKAKEAC
TCRMTGPGKHKCECKSHYVGD 1025	Qy 975 CKKGYKGDGYSCIEIDPCADGVNGGCHEHATCRMTGPGKHKCECKSHYVGD
KCSOKGTQVSCS 974	Qy 924 ATCTENNTCVCNLNYEGDGITCTVVDFCKQNNGGCAKVAKCSQKGTQVSCS
VFAVCTPACSVH 923 	Qy 864 LCWHGRFGPDCQPRSCSEHGQCDEGITGSGECLCETGWTAASCDTPTAVFAVCTPACSVH
LCHTGFNGTACE 863	Qy 809 VIQTPROCHGYFMPDCQACPGGPDTPCNNRGMCRDLYTPMGQCLCHTGFNGTACE : : :
VEGCONLCTV 808 :: : IDECQNGPVCQ- 1819	Qy 759 TFDIPGECGSCIFTPKCPLKSKPKGVKKKCIYN-PLPFRRNVEGCQNLCTV :
1771	Db 1752 RPGFVIDIYTGLPVDIDECR

	SKEC-PKDGCGDGYECDAAIGCCHVDOMSCGKAKQEFE 898	862	Db	
	EPEQLPLDRCLQDNGQCHPDASCADLYFQDTTVGVFHL-RSPLGQYKLTFD 1079	1030	Qy	
861	DKPCEDGYYGPDCIKKCKCQGTATSSCNRVSGACHCHPGFTGEFCHALCPESTFGLKC	804	Db	
102	Ð	987	Qy	
803	VCRCTSEYKQCNAQTGECSCPAGE	748	Db	
986	CVCNLNYEGDGITCTVVDFCKQNNGGCAKVAKCSQKGTQVSCSCKKGYKGDGYSC	932	Qy	
747	DGHGCDPTTGECICEPGYHGKTCSEKCPDGKYGYGCALDCPKCASGS	691	Db	
931	CSEHGQCDEGITGSGECLCETGWTAASCDTPTAVFAVCTPACSVHATCTE-NNT	879	Qy	
690	SCPPGSSGIH	631	Db	
878	PCNNRG-MCRDLYTPMGOCL-CHTGFNGTACE-LCWHGRFGPDCQP-RS	834	Qy	
630	YGESCELSCPCSDASCSKQTGKCLCPLGTKGVSCDQ	595	рb	
833	VKKKCIYNPLPFRRNVEGCQNLCTVVIQTPRCCHGYFMPDCQACPGGPDT	784	Qy	
594	ANCDIGCPEGSYGPGCKLHCKCVNGKCDKETGEC-TCQPGFFGSDCSTTCSKGK-	542	Db	
783	LLFDVGVAYGIDCLLMNPTLGGRCDTFTTFDIPGECGSCIFTPKCPLK-SKPKG	731	Qy	
541	GANCEKRCKCPKGIGCDPITGECTCPAGLQG	511	Db	
730	KSYLKFHVIRDSKALASDLPRSASWKTLQGSELSVRCGTGSDIG-ELFLNEQMCRFIHRG	672	Qy	
510	RCEHHCPADTE	500	Db	
671	AANHGYTKFSKLIQDSGLLSVITDSIHTPVTVFWPTDKALEALPPEQQDFLFNQDNKDKL	612	Qy	
499	GADGKCQCDRGWTGH	485	Db	
611	VSISVSQDTVFINNEAKVLSSDIISTNGVIHVIDKLLSPKNLLITPKDALGRVLQNLTTV	552	Qу	
484)CQCN	461	Db	
551	GPFTVFAPLSSSENHEPRIKDWDQQGLMSQVLRYHVVGCQQLLLDNLKVTTSATTLQGEP	492	Qу	
460	DWNHASECNPETGSCVCKPGRTGKNCSE	432	Db	
491	NYTEODQRICTCKPDYTGDGIVCRGSIYGELPKNPSTSQYFFQLQEHAVRELAGP	437	Qy	
431	YGADCSKTCTCVRENTLMCAPNTGFCRCKPGFYGDNCELACSKDSYGPNCEKQAMC	376	DЬ	
436	TNNGGCSPFAFC	385	Qy	
375	DIGCSRGRFGLOCKONCTCPGLEFSDSNASCDAKTGQCQCESGYKGPKCDERKCDAEQ	318	Db	
384	DGIVCLEINPCLEN	345	Qy	
317	VGFFGSGCTQKCDCLNNQN	258	Db	
344	LDPDGKASCKCAAGFRGNGTVCTAINACETSNG	312	Qy	
257	CNKEGKCVCSDGWGGEFCLNKCEEGKFGAECKFECNCQNGATC-	210	Db	
311	VH-GRCSQGPLGDGSCDCDVGWRGVKCDMEITTDNCNGTCHTSANCL	266	Qy	
209	GPNCVKSCPC	150	Db	
265	LGTASVWDGVNGTGTCQCGLGFNGTACE-TCTEGKYGIHCDQACSC	221	Qy	

RESULT 12 A49175 Motch B protein - mouse (fragment) N;Alternate names: Notch homolog

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A; Molecule type: mRNA
A; Residues: 1-1203 < LAR>
A; Residues: 1-1203 < LAR>
A; Cross-references: EMBL; X68279; NID:g287989; PIDN:CAA48340.1; PID:g287990
A; Experimental source: embryo
A; Note: sequence extracted from NCBI backbone (NCBIP:126158)
C; Comment: This protein has many EGF repeats and lin-12/Notch repeats.
C; Comment: This protein is one of the neurogenic proteins controlling the decision betwee C; Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
C; Superfamily: EGF homology < EGX1>
F; 143-174/Domain: EGF homology < EGX1>
F; 143-174/Domain: EGF homology < EGX1>
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C;Date: 21-Jan-1994 #sequence_revision 05-Jan-1996 #text_change 20-Sep-1999
C;Accession: A49175, pH1570; S32113
R:Lardelli, M.: Lendahl, U.
Exp. Cell Res. 204, 364-372, 1993
A:Title: Motch A and Motch B--two mouse Notch homologues coexpressed in a wide variety A:Reference number: A49175; MUID:93178563
A:Accession: A49175
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F;560-591/Domain: EGF homology
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712-743/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 TDGAFHCECLKGYAGPRCEMDI -- NECHSDPCQNDATC - LDKIGGFTCLCMPGFK -- GVH 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           276 GDGS--CDCDVGWRGVKCDMEITTDNCNG-TCHTSANCLLDPDGKASCKCAAGFRGNGTV 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       219 CALGTASVWDGVNGTGTCQCGLGFNGTACETCTEGKYGIHCDQACS--CVH-GRCSQGPL 275
556 DVDECISKPCMNNGVCHNTQGSYVCECPPGFSGMDCEEDINDCLANP---
                                                 778 K----SKP---KGV-----
                                                                                                                                                                                                                                                                                                                                                                    617 YTKFSKLIQDSGLLSVITDSIHTPVTVFWPTDKALEALPPEQQDFLFNQDNKDKLKSYLK 676
                                                                                                                                                                                                                                                                                                                                                                                                                           367 DE----CASNPCRKGATCINDVNGFRCICPEGPHHPSCYSQVNECLSNPCIHGNCTGGLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                222 TPCLNGAKCID-HPNGYECQCATGFTG-----ILCDENIDNCDPDP-CHHGQCQDGI 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 CHKGALCDTNPLNGQYICTCPQGYKGADCTEDVD----ECAMANSNPCEHAGKCVN---
                                                                                                                                                                                                                                                              FHVIRDSKALASDLPRSASWKTLQGSELSVRCGTGSDIGELFLNEQMCRFIHRGLLFDVG 736
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                                                                                                                                                     VAYGIDCLLMNPTLGGRCDTFTTFDIPGECG------SCIFTP-----KCPL 777
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                                                                                                      SGYTCHCML - - PYTGKNCQTVLAPCSPNPCENAAVCKEAPNFESFSCLCAPGWQGKRCTV
                                                                                                                                                                                                         ------RCTCKKGFKGYNCQV-----NIDECASNP--C--LNQGTCFDDV 497
                                                                                                                                                                                                                                                                                                               Y----KCLCDAGWYGVNCE-------VDKNECLSNPCQNGGTCN----NLVNGY--
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EGF homology
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DGI 373	DGKASCKCAAGFRGNGTVC-TAINACETSNGGCSTKADCKRTTPGNRVCVCKAGYTG	315	Qy
359	ARGATCDTNP1TGHWMCDCPDGWTDKDCSKDIDECSLGGNPCEHNGQCNNT	309	Db
JDP 314	VHG-RCSQGPL-GDGSCDCDVGWRGVKCDMEITTDNCNGTCHTSANCLLDD	266	Оy
DPC 308	CNCVYGFTRDDCSENIDDCSNVACFHNARCIDQAGTFECLCTPGNRILCHLDDACISDPC	249	Db
-SC 265	CQCGLGFNGTACETCTEG-KYG1HCDQAC	236	Qy
FT 248	NGATCADAVSTYDCHCPAEWTGQYCTIDVDECSLSNNVAKRRDLQQTEGGFT	197	Db
IGT 235	PQCVRTIITRACWLASLAHNAKPAPGEVKMCALGTASVWDGVNGTGT	189	Qy
-co 196	NECDTPDICQNAGTCSNNDGGYSCSCVAGFEGNNCEVNIDDCSGHS	149	Db
3CQ 188	NRCDNNDTIIVRGECGKCSQQAPCPLETKPLRETRKCIYSIYFMGKRSVFIG	135	Qy
Gaps 67;	Match 6.0%; Score 474.5; DB 2; Length 2352; Local Similarity 21.5%; Pred. No. 4.7e-21; No. 275; Conservative 97; Mismatches 440; Indels 467;	Query M Best Lo Matches	M B O
Plun: BAAZ33/1.1	erences: EMBL:ABUU132/; N1D:Q12044/2; P1D:Q1028001; ch	;Cross-rei ;Genetics; ;Gene: Not	A; q;
1	R>	A; Molecule 'A; Residues:	A; Mo
	A;Accession: T30201 A;Status: preliminary; translated from GB/EMBL/DDBJ	A;Accession: A;Status: pro	A; A; A; S:
expressed in the	thia roretzi is preferentially	itle: eferer	A; T: A; R
	M.; Makabe, K.W. 7	ori, s . Gene	R; Ho
sep-2000	n 02-Sep-2000 #text_change 02-S	ate: (C; D;
	olog protein - sea squirt (Halocynthia roretzi) : Halocynthia roretzi	ch hor	Not
	ù.	ULT 1	RESI
	NCICRSAFTGRHCETFLDVCPQKPCLNGGTCAVASNMP	972	Dъ
		1161	Qy
NY 971	PHCLNGGQCVDRIGGYTCRCLPGFAGERCEGDINECLSNPCSSE-GSLDCVQLKN	916	Db
DV 1160	YHLCSAGWLESGRVAYPTTYASQKCGANVVGIVDYGSRANKSEMWDVFCYRMK-	1106	Qу
-GG 915	CQNGGTCIDLVNHFKCSCPPGTRGLLCEENIDECA	879	рb
(AK 1105	CHPDASCADLYFQDTTVGVFHLRSPLGQYKLTFD	1046	Qy
IQP 878	EEQLDECASNPCQHGATCN-DFIGGYRCECVPGYQGVNCEYEVDECQNQP	830	DЪ
IGQ 1045	CIEIDPCADGVNGGCHEHATCRMTGPGKHKCECKSHYVGDGVDCEPE	986	Qy
YC 829	DGAYCDVLNVSCKAAALQKGVPVEHLCQHSGICINAGNTHHCQCPLGYTG-SYC	777	DЬ
YS 985	DGITCTVVDF-CKQNNGGCAKVAKCSQKGTQVSCSCKKGYKGDGYS	941	Qy
1 776	CVDGL-GTYRCICPLGYTGKNCQTLVNLCSRSPCKNKGTCVQEKARPHCLCPPGW	723	Db
EG 940	CDEGITGSGECLCETGWTAASCDTPTAVFAVCTPA-CSVHATCTENNTCVCNLNYEG	885	Qy
GT 722	HGVHCENNIDECTESSCFNGGTCVDGINSFSCLCPVGFTGPFCLHDINECSSNPCLNAGT	663	Db
IGQ 884		858	Оy
GF 662	G	607	рb
GF 857	-LCTVVIQTPRC-CHGYEMPD-CQACPGGPDTPCNNRGMCRDLYTPMGQCLCHTGF	805	Qy

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                             KAGYVGDGFSCSGNLLQVL 1183
                                                                                                                            CNDL-----INSYSCICALGYEGATCLTDKDECASSP--
                                                                                                                                                             CADLYFODTTVGVFHLRSPLGQYKLTFDKAKEACAKEAATIATYNQLSYAQKAKYHLCSA 1111
                                                                                                                                                                                             CLNG--GTCHDTSTA-----HECSCVAGFTGSYCD----IDIDECA--SVPCKNGAT 1085
                                                                                                                                                                                                                           CADGVNGGCHEHATCRMTGPGKHKCECKSHYVGDGVDCEPEQLPLDRCLQDNGQCHPDAS 1051
                                                                                                                                                                                                                                                                                             TVVDFCKQNNGGCAKVAKCSQKGTQVSCSCKKGYKGD-------GYSCIEI---DP
                                                                                                                                                                                                                                                                                                                            SYSCSCTANFTGDKCQNAVNNCASLQCQNGGTCYYDSGDPKCACVHGYTGTHCESLQNLC
                                                                                                                                                                                                                                                                                                                                                                NNTCVCNLNYEGD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            GYQCTCSQGFTGKDCDTDI-----DDCSSNPCLNGGQCLDDV-GSYKCLCLPGFEGNNCQ 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGQCLCHTGFNGTACELCWHGRFGPDCQPRSCSEHGQCDEGITGSGECLCETGWTAASCD 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------TFTTFDIP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIQECSSNPCLHEYARRDQHVHCICDAGY-QGENCETEINECASNPCQHGACENKVAQFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIGEL ---- FLNEQMCRFIHRGLLFDVGVAYGIDC ----- LLMNPTLGGRCD -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DFLFNQDNKDKLKSYLKFHVIRDSKALASDLPRSASWKTLQGSELSVRCGTG-----S 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALGRVLQNLTTVAANHGYTKFSKLIQDSGLLSVITDSIHTPVTVFWPTDKALEALPPEQQ 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTSGSSCE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VC-----LEINPCLENHGGCDRNAECTQTGPNQAVCNCLPKYTGDGKVCSL-INVCLTN 426
PSGY -- EGRRCQGDVNECL 1190
                                                             GGTCIDRI -- NSFYCS -- CLAGTEGVL-
                                                                                            GWLESGRVAYPTTYASQKCGANVVGIVDYGSRANKSEMWDVFCYR-----MKDVNCTC 1164
                                                                                                                                                                                                                                                             TGPNICK--NGG-----SCVQTSNTVSCNCLGGYEGTDCAVPQVSCTVGASLLGIAVSDL 1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PC---ENGATCQESADYLAYVCQCPEGFRGPTCATDINEC---VNSPCKNGGGCTNL-VP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLPFRRNVEGCONICTVVIQTPRCCHGYFMPDC----QACPGGPDTPCNNRGMCRDLYTP 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHCDAGYTGTACEIDINECATQPCQNGGTCTSGINSYNCACPAKYTGVNCETELSPCVPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VTTSATTLQGEPVSISVSQDTVFINNEAKVLSSDIISTNGVIHVIDKLLSPKNLLITPKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --PCMNKATC-IDKANAYECECAPGYTGVHCETNIDDCVINPCHYGSCRDGVNTFYCDCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NGGCSPFAFCNYTEQDQRICTCKPDYTG-----DGIVCRGSIYGELPKNPSTSQYFFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LQEHAVRELAGPGPFTVFAPLSSSFNHEPRIKDWDQQGLMSQVLRYHVVGCQQLLLDNLK 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ICDEDIDECESNPC-ANGGTCIDEV-----NAYTCSCALGFTGDD--CSQNIDECAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----GECGSCIFTPKCPLKSKPKGVK----KKCIYN 791
                                                             -CEINEDECEINICLNGGVCIDGIGGFSCQC
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RESULT

14

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transmembrane protein precursor - zebra fish
C;Species: Brachydanio rerio (zebra fish)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Sep-1999
C;Accession: $42612
R;Bierkamp, C; Campos-Ortega, J.A.
Mech. Dev. 43, 87-100, 1993
A;Title: A zebrafish homologue of the Drosophila neurogenic gene Notch and iA;Reference number: $42612; MUID:94128602
A;Accession: $42612
A;Status: preliminary
A;Status: preliminary
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F;1185-1216/Domain: EGF homology <EGF2>
F;1915-1947/Domain: ankyrin repeat homology
F;19148-1980/Domain: ankyrin repeat homology
F;1982-2014/Domain: ankyrin repeat homology
F;2015-2047/Domain: ankyrin repeat homology
F;2048-2080/Domain: ankyrin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X69088; NID:g433866; PIDN:CAA48831.1; PID:g433867 C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; F;755-786/Domain: EGF homology <EGF1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-2437 <BIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.0%;
Best Local Similarity 20.3%;
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                                                                                                                                                                      DGVASFTCDCRPGYTGR--LCETNI-NECLSQPCRNGGTCQDRENAYICTCPKG-----
                                                                                                                                                                                                                                                                                                                                                                                      VCVCKAGYTGDGIVCLEIN-----PCL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTHTCSCLPGFTGQTCEHNVDDCTQHACENGGPCIDGINTYNCHCDKHWTGQYCTEDVDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NPCANG-----GQCSAFESHYICTCPPNFHGQTCRQDVNECAVSPSPCRNGGTCINEV- 198
                                                                                                                                                                                                                QRI----CTCKPDYTGDGIVCRGSIYGELPKNPSTSQYFFQLQEHAVRELAGPGPFTVFA 498
                                                                                                                                                                                                                                                            ASTPCKNGAKCTD-GPNKYTCECTPGFSGIH--CELDINECAS----SP---CHYGVCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CELSPNACQNGGTCHNTIGGFHCVCVNGWTGDDCSENI--DDCASAACSHGATCHDRVAS
                                       DTVFINNEAKVLSSDIISTNGVIHVIDKLLSPKNLLITPKDALGRVLQNLTTVAANHGYT
                                                                                                                           PLSSSFNHEPRIKDWDQQGLMSQVLRYHVVGCQQLLLDNLKVTTSATTLQGEPVSISVSQ
                                                                                                                                                                                                                                                                                                    ----CDRNAECTQTGPNQAVCNCLPKYTGDGKVCSL-INVCLTNNGGCSPFAFCNYTEQD
                                                                                                                                                                                                                                                                                                                                       HCICMPGY--EGVFC-QINSDDCASQPCLNGKCIDKINSFHCECPKGFSGSLCQVDVDEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----SCVHGRCSQGPLGDGSCDCDVGWRGVKCDMEITTDNC-----NGTCH----
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                                                                                                                                                                                                                                                                                                                                                                                                                              ECSLGANPCEHGGRCLNTKGSFQCKCLQGYEGPRCEMDVNECKSNPCQNDATCLDQIGGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----AINACETSNGGCSTKA--DCK-------RTTP------GNR 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FFCECPHGRTGLLCHLDDACISNPCQKGSNCDTNPVSGKAICTCPPGY--TGSACNQDID 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FMGKRSVFIGCQPQ-----CVRTIITRACWLASLAHNAKPAPGEVKMCALGTASVWDGVN 231
INGYECVCEPGYSGSMCNINIDDCALNPCHNGGTCIDGV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             )%; Score 473.5; DB 2;
3%; Pred. No. 5.6e-21;
123; Mismatches 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----TSANCLLDP-DGKASCKCAAGFRGNGTVCT----
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  -NSFTCLCPDGF-
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90;

RESULT T1954 MEGF6 1 C; Spec C; Date C; Acces R; Naka Genomi A; Titll A; Refe A; Acces A; Role A; Role A; Rosi A; Resi A; Cross A; Expes	Db Oy	оу Оу	Qy Db	Qy Db	Db Qy Db	Оу ДЪ Оу	0y 0b	Oy Oy Db
RESULT 15 T13954 MEGF6 protein - rat C;Species: Rattus norvegicus (Norway rat) C;Apecies: Rattus norvegicus (Norway rat) C;Species: Rattus norvegicus (Norway rat) C;Species: Rattus norvegicus (Norway rat) C;Apecies: Rattus norvegicus (Norway rat) C;Apecies: Rottus norvegicus (Norway rat) C;Apecies: Rottus norvegicus (Norway rat) C;Apecies: Tigeta norvegicus (Norway rat) R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O. Genomics 51, 27-34, 1998 R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O. Genomics 51, 27-34, 1998 A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs A;Reference number: Z14126; MUID:98360089 A;Reterence number: Z14126; MUID:98360089 A	1129 KCGANVVGIVDYGSRANKSEMMDVFCYRMKDVNCTCKAGYVGDGFSCSGNLLQVLM 1184	KCECKSHYVGDGYDCEPFOLPLINGLODINGQCHDASCADLYFQDTTYGVFHLKSPLG	LVNTYKCSCPRGTOGVHCEIDIDDCSPSVDPLTGEPRCFNGGRCVDRVGGY	896 LCETGWTAASCDTPTAVFAVCTPACSVHATCTENNTCVCNLNYEG 940	874 -CQPRSCSEHGQCDEGITGSGEC 895	VCQDRVNGFVCVCLAG	799 -LNOGSCIDDVAGFKCNCMLPYTGEVCENVLAPCSPRPCKNGGVCRESEDFOSFSCNC 855 776 PLKSKPKGVKKKCIYNPLPFRRNVEGCQNLCTVVIQTPRCCHGYF 820 1	19 KFSKLIQDSGLLSVITDSIHTPVTVFWPTDKALEALPPEQODFLFNQDNKDKLKSYL : : : : : 07RDATCLSQHNECSSNP
OY 717 LFLNEDWCREIHRGLLEDVGVA	Qy 606 QNLTTVAANHGYKFSKLIQSGLLSVITDSIHTPVTVFWPTDKALEALPPEQODFLF 663	503 SFNHEPRIKDWDQQGLMSQVLRYHVVGCQQLLLDNLKVTTSATTTLQGEPVSISVSQDTVF	458 VCRGSIYGELPKNPSTSQYFEQLQEH-AVRELAGPGPET-VFAPLSS i	Qy 358 GNRYCYCKAGYTGDGIYCLEINPCLENHGGCDRNAECTQTGPNQAVCNCLPKY- 410	Db 239 QEDGRRCVRRSPCAEGNGGCMHICQELRGLAHCGCHPGYQ-LAADRKTCEDVDECALGLA 297 Qy 305 HTSANCLLDPDGKASCKCAAGFRGNGTVCTAINACETSNGGCSTKADCKRTTP 357	Qy 231 NGTGTCQCGLGFNGTACETCTEGKYGIHCDQACSCVHGRCS 271	Db 74 CAQQAWCIGQERRIVYYMSYRQVYATEARTVFRCCPGWSQKPGQEGCLSDVDEC 127 Qy 186GCQPQCVRTIITRACWLASLAHNAKPAPGEVKMCA-LGTASVWDGV 230 Qy 186GCQPCVRTIITRACWLASLAHNAKPAPGEVKMCA-LGTASVWDGV 230	Genetics: Gene: MEGF6 6.0%: Score 473; DB 2; Length 1574; Query Match Best Local Similarity 22.4%; Pred. No. 3.5e-21; Matches 300; Conservative 99; Mismatches 460; Indels 478; Ga

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1156 RMKDVNCTCKAGYVGDG 1172
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1233 PASGV-CTCAAGYHGTG 1248
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                                                                                                                          1115 TGDKCQSSCVSGTFGVHCEEHCACRKGASCHHVTGACFCPPGWRGPHCEQACPRGWFGEA 1174
                                                                                                                                                                                     1175 CAQRCLCPTNASCHHVTGECRCPPGFTGLSCEQACQPGTFGKDCEHLCQCPGETW--ACD 1232
                                                                                                                                                         1077 TFDKAKEACAKEAATIATYNQLSYAQKAKYH------LCSAGWLESG 1117
                                                                                                                                                                                                                                                                                                                  963 ACNCSAGAPCDAVTGSCICPAGRWGPRCAQSCPPLTFGLNCSQICTC-FNGASCDSVTG- 1020
                                                                                                                                                                                                                                                                                                                                                 919 A--CSVHATC-TENNTCVCNLNYEGD------GITCTVVDFCKQNNGGCAKVAKC 964
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Search completed: June 17, 2002, 12:31:15 Job time: 281 sec

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Result
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Q90yd2 xenopus lae	Q90YD2	13	1214	5.2	406	45
Q90819 gallus gall	090819	13	1193	5.2	410	44
റ	Q19350	ű	1722	5.2	411.5	43
	Q21281	υ	2104	5.3	413.5	42
Q9vb65 drosophila	Q9VB65	υ	1404	5.3	414.5	41
Q90y57 brachydanio	Q90Y57	13	1242	5. 3	415	40
Q96jp8 homo sapien	Q96JP8	4	2809	υ. 3	420.5	39
035452 mus musculu	035452	11	4006	5.4	421	38
caen	Q964N4	υ	2104	5.4	423.5	37
homo	Q96KG7	4	1140	5.4	424.5	36
Q9npk9 homo sapien	Q9NPK9	4	4288	5.5	430	35
dros	Q9VM55	G	3396	5.5	431	34
Q96kg6 homo sapien	Q96KG6	4	969		431	33
018977 bos taurus	018977	6	4135		434	32
035442 mus musculu	035442	11	1964	5.6	437.5	31
	013149	13	2447		443	30
	Q9R172	11	2319	5.7	447	29
Þ	Q9H240	4	2471	5.7	450.5	28
homo	204721	4	2471	5.7	450.5	27
lyte	016004	υī	2531	5.7	452	26
_	Q9VR08	ъ	3680	5. 8	453.5	25
000306 homo sapien	000306	4	2003		459.5	24
	099940	4	1999	•	461.5	23
0 rat	Q9QW30	11	2471		465	22
· 	Q9UM47	4	2321	6.0	469	21
homo	0916L8	4	2321		469	20
Q9upl3 homo sapien	Q9UPL3	4	2281	•	469	19
1 rati	088281	11	1574	6.0	473	18
O61240 halocynthia	061240	Ŋ	2352	6.0	474.5	17

ALIGNMENTS

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InterPro; IPRO00782; BIGH3_fasciclin.
InterPro; IPRO00561; EGF-1ike.
InterPro; IPRO002049; Laminin_EGF.
InterPro; IPR002049; Link
Pfam; PF00098; EGF; 9.
Pfam; PF00193; Xink; 1.
Pfam; PF00193; Xink; 1.
PRINTS; PR0011; EGFLAMININ.
PRINTS; PR01265; LINKMODULE.
PRODOm; PD000918; Link; 1.
SMART; SM00181; EGF; 9.
SMART; SM00445; LINK; 1.
PROSITE; PS00022; EGF]; UNKNOWN_1.
PROSITE; PS00022; EGF]; UNKNOWN_1.
PROSITE; PS00022; EGF]; UNKNOWN_1.
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O9H7H7;
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FLJ00112 PROTEIN (FRAGMENT).
FLJ00112.
                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                                                                                                                                                                                               Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AK024503; BAB15793.1; -. HSSP; P98066; ITSG.
                                                                                                                                                                                                                                                                           spleen."
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"The nucleotide sequence of a long cDNA clone isolated from human
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                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
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   1192 AA;
   128738 MW;
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SFYNDLVNGTFLRTMLGSQLLITFSQDQLH-QETRFVDGRSILQWDIIAANGILHIISEP
                                      NFLTEVLAFSKSSARGQAFLKHLTDLSIRGTLFVDQNSGLDGNKSLSGRDIEHHLTNVNV
                                                                                      GANVVGIVDYGSRANKSEMWDVFCYRMKDVNCTCKAGYVGDGFSCSGNLLQVLMSFPSLT
                                                                                                                                       LGQYKLTFDKAKEACAKEAATIATYNQLSYAQKAKYHLCSAGWLESGRVAYPTTYASQKC 1130
                      NFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENETLSGRDIEHHLANVSM
                                                                        GSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNCTCKVGYVGDGFSCSGNLLQVLMSFPSLT
                                                                                                                                                                                                                                    CKQNNGGCAKVAKCSQKGTQVSCSCKKGYKGDGYSCIEIDPCADGVNGGCHEHATCRMTG
                                                                                                                                                                        PGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHLRSP 846
                                                                                                                                                                                                                         CKQDNGGCAKVARCSQKGTKVSCSCQKGYKGDGHSCTEIDPCADGLNGGCHEHATCKMTG
                                                                                                                                                                                                                                                                                    GSGECLCETGWTAASCDTPTAVFAVCTPACSVHATCTENNTCVCNLNYEGDGITCTVVDF
                                                                                                                         LGQYKLTFDKAREACANEAATMATYNQLSYAQKAKYHLCSAGWLETGRVAYPTAFASQNC
                                                                                                                                                                                     PGKHKCECKSHYVGDGVDCEPEQLPLDRCLQDNGQCHPDASCADLYFQDTTVGVFHLRSP 1070
                                                                                                                                                                                                                                                                        GSGQCLCETGWTGPSCDTQAVLPAVCTPPCSAHATCKENNTCECNLDYEGDGITCTVVDF
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Best Local Similarity 73.1%;
Matches 798; Conservative 100
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Pfam; PF00008; EGG; 8.

Pfam; PF00193; Xlink; 1.

PF1am; PF00193; Xlink; 1.

PRINTS; PR001918; LinkMODULE.

PRINTS; PR00011; EGF; 1.

PRODOM; PD000918; Link; 1.

SMART; SM00181; EGF; 8.

SMART; SM00181; EGF; 1.

SMART; SM00181; EGF; 1.

SMART; SM00181; EGF; 1.

PROSITE; PS01022; EGF; 1; UNKNOWN_2.

PROSITE; PS010248; LAMININ_TYPE_EGF; 1.

PROSITE; PS01248; LAMININ_TYPE_EGF; 1.

EGF-like domain; Glycoprotein; Hypothetical profile of the comain of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blum H., Bauersachs S., Mewes H.W., Gassenhuber J., Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databb EMBL, AL133021; CAB61358.1; -- HSSP, P98066; ITSG.
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01-MAY-2000 (TrEMBLrel 13, Last sequence update)
01-DEC-2001 (TrEMBLrel 19, Last annotation update)
HYPOTHETICAL 115.7 KDA PROTEIN (FRAGMENT)
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1147
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InterPro; IPR000561; EGF-like.
InterPro; IPR002049; Laminin_EGF.
InterPro; IPR000538; Link.
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VFAPLSAAFDEBARVKDWDKYGLMPQVLRYHVVACHQLLLENLKLISNATSLQGEPIVIS
                                         VFAPLSSSFNHEPRIKDWDQQGLMSQVLRYHVVGCQQLLLDNLKVTTSATTLQGEPVSIS
                                                                                                                                                                                        LRAPPTAATAAHSGLGTGIFCAVVLVTGATALAAYSYFRLKQRTTGFQRFDQKRTLMSWL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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100; Mismatches
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CD44-LIKE PRÉCURSOR FELL. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; NCBI_TaxID=9606;
                                                        O9NRY3; PRELIMINARY;
Q9NRY3;
01-OCT-2000 (TrEMBLrel. 15,
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Best Local S
Matches 676
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Pfam; PF02469; Fasciclin; 1.

PRINTS; PR01265; LINKMODULE.

ProDom; PD000918; Link; 1.

SMART; SM00181; EGF; 5.

SMART; SM00181; EGF; 5.

SMART; SM00445; LINK; 1.

PROSITE; PS00122; EGF_1; UNKNOWN_2.

PROSITE; PS01186; EGF_2; 4.

PROSITE; PS01148; LAMTNIN_TYPE_EGF; 1.

PROSITE; PS01248; LAMTNIN_TYPE_EGF; 1.
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Tao Q., Zhang W., Cao )
"Molecular cloning and
with CD44.";
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             VAYPTTYASQKCGANVVGIVDYGSRANKSEMMDVFCYRMKDVNCTCKAGYVGDGFSCSGN
                                                                                                                                                                                    EGDGITCTVVDFCKQNNGGCAKVAKCSQKGTQVSCSCKKGYKGDGYSCIEIDPCADGVNG
                                                                                                                                                                                                                                             CSEHGOCDEGITGSGECLCETGWTAASCDTPTAVFAVCTPACSVHATCTENNTCVCNLNY
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676; Conserv
VAYPTAFASQNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNCTCKVGYVGDGFSCSGN
                                                                                                                                                                       EGDGITCTVVDFCKQDNGGCAKVARCSQKGTKVSCSCQKGYKGDGHSCTEIDPCADGLNG
                                                                                                                                                                                                                                CSDHGQCDDGITGSGQCLCETGWTGPSCDTQAVLPAVCTPPCSAHATCKENNTCECNLDY
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76.18;
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Pred. No. 0;
87; Mismatches
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MEDIINE-9719134; PubMed-9039502;
Nagase T., Seki N., Ishikawa K., Ohira M., Kawarabayasi Y., Ohara Tanaka A., Kotani H., Miyajima N., Nomura N.;
Tanaka A., Kotani H., Miyajima N., Nomura N.;
"Prediction of the coding sequences of unidentified human genes.
the coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced analysis of cDNA clones from cell line KG-1 and brain.";
DNA Res. 3:321-329(1996)
DNA Res. 3:321-329(1996)
EMBL; D87433; BAA13377.1; -.
HSSP; P98066; 1TGG.
                                                                                                                                                                                                                                                                                                   PROSITE;
PROSITE;
PROSITE;
EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD000918; Link; 1.
SMART; SM00180; EGF_LLam; 1.
SMART; SM00001; EGF_Like; 13.
SMART; SM00445; LINK; 1.
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01-FEB-1997 (TrEMBLrel. 02,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pfam; PF00008; EGF; 13.
pfam; PF02469; Fasciclin; 3.
pfam; PF00193; Xlink; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR000782; BIGH3_fasciclin.
Interpro; IPR001128; Cyt_P450.
Interpro; IPR000561; EGF-like.
Interpro; IPR0002049; Laminin_EGF.
Interpro; IPR000238; Link.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR01265; LINKMODULE. ProDom; PD000918; Link; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
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EGF_2; 13.
LAMININ_TYPE_EGF;
                                                                                                                                                                                                                                                                                                                          LINK; UNKNOWN_1
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40.28;
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SDAMCTDLHFQEKRAGVFHLQATSGPYGLNFSEAEAACEAQGAVLASFPQLSAAQQLGFH
                  PDASCADLYFQDTTVGVFHLRSPLGQYKLTFDKAKEACAKEAATIATYNQLSYAQKAKYH
                                                                                       IDPCADGVNGGCHEHATCRMTGPGKHKCECKSHYVGDGVDC-EPEQLPLDRCLQDNGQCH 1047
                                                                                                                                                             NNTCVCNLNYEGDGITCTVVDFCKQNNGGCAKVAKCSQKGTQVSCSCKKGYKGDGYSCIE
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                                                                  RNPCTDGHRGGCSEHANCLSTGLNTRRCECHAGYVGDGLQCLEESEPPVDRCLGQPPPCH
                                                                                                                                         GNSCECSLGYEGDGRVCTVADLCQDGHGGCSEHANCSQVGTMVTCTCLPDYEGDGWSCRA
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                                                                                                                                                                                                                                     Pfam; PF00008; EGF; 18.

R Pfam; PF002469; Fasciclin; 4.

R Pfam; PF00193; X1ink; 1.

R Pfam; PF00193; X1ink; 1.

R PRINTS; PR00011; EGFLAMININ.

PPCDOM; PD000918; Link; 1.

R SMART; SM00180; EGF_Lim; 1.

R SMART; SM00001; EGF_Like; 15.

R SMART; SM000445; LINK; 1

R PROSITE; PS00186; CYTOCHROME_P450; UNKNOWN_2.

PROSITE; PS00122; EGF_1; UNKNOWN_7.

R PROSITE; PS01186; EGF_2; 16.

R PROSITE; PS01248; LAMINIT_TYPE_EGF; 2.

R PROSITE; PS01248; LAMINIT_TYPE_EGF; 2.

R PROSITE; PS01241; LINK; UNKNOWN_1.

EGF-like domain; Glycoprotein; Laminin EGF-like domain; Rej

SEQUENCE 2570 AA; 275345 MW; 3123FABD7C8E2BF8 CRC64;
                                                                                                          Query Match 35.7%; S
Best Local Similarity 40.0%; P
Matches 561; Conservative 222;
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Q9NY15;
Q1-OCT-2000
01-OCT-2000
01-DEC-2001
STABILIN-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; V
Mammalia; Eutheria; Primates; Catarrhini;
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InterPro; IPR002049;
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  LLQQLDLVPAFSLFRELLQHHGLVPQIEAATAYTIFVPTNRSLE---AQGNSSHLDADTV 1187
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IPR001128; Cyt_P450.
IPR000561; EGF-like.
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 19, Last annotation updat
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                              SDAMCTDQHFQEKRAGVFHLQATSGFYGLNFSEAEAACEAQGAVLASFPQLSAAQQLGFH
                                                  PDASCADLYFQDTTVGVFHLRSPLGQYKLTFDKAKEACAKEAATIATYNQLSYAQKAKYH
                                                                                                                                                            GNSCECSLGYEGDGRVCTVADLCQDGHGGCSEHANCSQVGTMVTCTCLPDYEGDGWSCRA
                                                                                                                                                                                                                             AFGPHCQACRCTVHGRCDEGLGGSGSCFCDEGWTGPRCEVQLELQPVCTPPCAPEAVCRA
                                                                                                                                                                                                                                                                                             {\tt TTWKPSCCPGHYGSECQACPGGPSSPCSDRGVCMDGMSGSGQCLCRSGFAGTACELCAPG}
                                                                                                                                                                                                                                                                                                          VIQTPRCCHGYFMPDCQACPGGPDTPCNNRGMCRDLYTPMGQCLCHTGFNGTACELCWHG
                                                                                                                                                                                                                                                                                                                                                                                                                        PGELMVGEDDARIVQRHLPFEGGLAYGIDQLLEPPGLGARCDHFETRPLRLNTCSICGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LITPKDALGRVLQNLTTVAANHGYTKFSKLIQDSGLLSVITDSIHTPVTVFWPTDKALEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INVCLTNNCGCSPFAFCNYTEQDQRICTCKPDYT-GDGIVCRGSIYGELPKNPSTSQYFF
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                                                                                                                                                                                                                                                           RFGPDCQPRSCSEHGQCDEGITGSGECLCETGWTAASCDTPTAVFAVCTPACSVHATCTE
                                                                                                                                                                                                                                                                                                                                                         PPCPEGSQEQGSPEACWRFYPKFWTSPPLHSLGLRSVWVHPSLWGRPQGLGRGCHRNCVT
                                                                                                                                                                                                                                                                                                                                                                                        PKCPLKSKPKGVKKKC-----IYNPLPFR----RNV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGELFLNEQMCRFIHRGLLFDVGVAYGIDCLLMNPTLGGRCDTFTTFDIP-GECGSCIFT 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPPEQQDFLFNQDNKDKLKSYLKFHVIRDSKALASDLPRSASWKTLQGSELSVRCGTGSD
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Matches 296; Conserv
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O9BI05, O1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000152; Asx_hydroxy1.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR000884; TSP1.
Pfam; PF00008; EGF; 24.
SMART; SM00101; EGF; 30.
SMART; SM00101; ASX_HYDROXYL; 22.
PROSITE; PS00010; ASX_HYDROXYL; 22.
PROSITE; PS01186; EGF_CA; 18.
PROSITE; PS01187; EGF_CA; 18.
PROSITE; PS01187; EGF_CA; 18.
Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
SEQUENCE 2189 AA; 224388 MW; C272A420B94FCBZD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-HOUGHTON;
Tomley F.M., Billington K.J., Bumstead J.M., Clark J.D., Monaghan P.;
"EtMIC4: A microneme protein from Eimeria tenella that contains tandem arrays of epidermal growth factor-like and thrombospondin type-I repeats.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ306433; CAC34726.1; -.
HSSP; P3555; IEMN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YVGDGFS-CSGNLLQVLMSFPSLTNFLTEVLAFSKSSARGQAFLKHLTDLSIRGTLFVPQ 1226
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   GYSGDGTA----QG---
                                                            GLGFNGTACETCTEGKYGIHCDQACSCV-----HGRCSQGPLGDGSCDCDVGWR--
                                                                                                                         -----CAR----GAC--NSLAHCKENPEGTAAIC-----TCIA 542
                                                                                                                                                                                  GKRSVFIGCOPOCVRTIITRACWLASLAHNAKPAPGEVKMCALGTASVWDGVNGTGTCQC 238
                                                                                                                                                                                                                                                                                                                                                                     7.7%; Score 603.5; DB 5; Length 2189; ilarity 24.3%; Pred. No. 2.3e-41; Conservative 114; Mismatches 459; Indels 347; Gaps
   HCDDIDECLAENDCTPADQGGICENTVGSYTCKCAAGYQQD
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404 CNCLPKYTODKVISLINNGCISPRECWYEDOORI-CTCKEDYTGDDIVCRGS DD 708 CECNBSEDGHKCEDVDPCGQGLHDCNWHAECSESDDNTTFKCTCGIGYTGEG	288 594 650 6708 708
CNCLPKYTGDGKVCSLINVCLTNNGGCSPFAFCNYTEQDORI-CI 	GVKCDMEITTDNC-NGTC:
FCNYTEQDORI-CTCKPDYTGDGIVCRGS 462	GVKCDMEITTDNC-NGTCHTSANCLLDPDGKASCKCAAGFRGNGTVCTAINACETSNG

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InterPro; IPR001557; Chitin_binding.

InterPro; IPR001561; EGF-Like.

InterPro; IPR00181; EGF-Like.

InterPro; IPR001821; TB.

InterPro; IPR001821; TB.

InterPro; IPR002212; CA.

SMART; SM00494; ChtBD2; 2.

SMART; SM00494; ChtBD2; 2.

SMART; SM00494; ChtBD2; 2.

R SMART; SM00494; EGF_Like; 4.

PROSITE; SM00491; EGF_Like; 4.

PROSITE; PS00101; ASX_HYDROXYL; 61.

PROSITE; PS001186; EGF_1; UNKNOWN_2.

R PROSITE; PS01186; EGF_2; 50.

R PROSITE; PS01187; EGF_CA; 61.

R PROSITE; PS001187; EGF_CA; 61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.1%; Score 557; DB 11; Length 3857; Best Local Similarity 20.6%; Pred. No. 5e-37; Matches 296; Conservative 136; Mismatches 403; Indels 600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-DEC-2001 (TrEMBLrel. 19, MUTANT FIBRILLIN-1.
           1426
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PGGYRCECDMGFVP--SADGKACEDIDECSLPNICVFGTCHNLPGLFRCECEIGYELDRS
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                                                             PNQAVCNC----LPKYTGDGKV-----CSLINVCL----
                                                                                                                                                                                                                                                                                                  KKGKTGCTDINECEIGAHNCGRHAVCTNTA-----GSFKCSCSPGWIGDGIKCTDLDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGEYRCLCYDGFMASEDMKTCVDVN---ECDLNPNICLSGTC-ENTKGSFICHCDMGYSG
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                                                                                                                                                   CSNGTHMCSQHADCKNTM-GSYRCLCKDGYTGDGFTCTDLDECSENLNLCG-NGQCL-NA
                                                                                                                                                                                         CETSNGGCSTKADCKRTTPGNRVCVCKAGYTGDGIVCLEINPCLENHGGCDRNAECTQTG
                                                                                                                                                                                                                                                                                                                                                    VK----C----DMEITTDNC--NGTCHTSANCLLDPDGKASCKCAAGFRGNGTVCTAINA
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32 DIDECSIPNICVFGTCHNLPGLFRCECEIG-YELDRSGGNC 2471	Db 243	
C DIPONICOCCUPATORING VECTORES CONTRACTORING COVER BEFORE VETTOR 100C	٠	
HI GDYSCLEIDPCADGVNGCHHATCRWTGPGKHKCEKSKYVGDGVDCEPBQL 1034	Оу 98 Дь 238	
CTNTAGSFKCSCSPGWIGDGIKCTDLDECSSGTHMCSQHADCKNTMGSYRCLCKDGYT 2	23	
ENNTCVCNLNYEGDG	Оу 92	
55 VDVNECDLNPNICLSGTCENTKGSFICHCDMGYSGKKGKTGCTDINECEIGAHNCDRHAV 2324	Db 2265	
105CSCDTPTAVFAVCTPACSVHAT 925	0у 9(
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70 FGPDCQPRSCSEHGQCDEGITGSGECLCETGWTAA 904	Оу 87	
	Db 214	
145ACE-LCWHGR 869	Оу 8	
8 ESGEMMMKNCMDIDECQRDPLLCRGGICHNTEGSYRCECPPGHQLSPNISACIDINE 2144	Db 2088	
120FM	Оу 87	
28 GKCRNTIGSFKCRCDSGFALDSEERNCTDIDECRISPDLCGRGQCVNTPGDFECKCDEGY 2087	Db 2028	
108VVIQTPRCCHGY 819	Qу 80	
SOUS SOUTH STREET S	Db 196	
PKCPLKSKPKGVKKKCIYNPLPFRRNVEGCQN	Оу 773	
)8 KNGLCVNSRGSFKCECPNGMTLDATGRICLDIRLETCFLKYDDEECTLPIAGRHRMDACC 1967	Db 1908	
67GSCIFT 772	Qy 76	
51 CCSSLGAAWGSPCTICQLDPICGKGFSRIKGTQCEDINECEVFPGVC 1907	Db 186	
23 MCRFIHRGLLFDVGVAYGIDCLL-MNPTLGGRCDTFTTFDIPGEC 766	Qy 73	
)7 CKNSPGSFICECSPESTLDPTKTICIETIKGTCWQTVIDGRCEININGATLKSE 1860	Db 1807	
67 NKDKLKSYLKFHVIRDSKALASDLPRSASWKTLQGSELSVRCGTGSDIGELFLNEQ 722	0у 6	
: : : : : : : : :	Db 1759	
6 GYTKFSKLIQDSGLLSVITDSIHTPVTVFWPTDKALEALPPEQQDFLFNQD	Qу 61	
11 NEC-ALDPD-TCPNGICENLRGTYKCICNSGYEVDITGKNCVDINECVLN- 1758	17	
U	Qу 56	
56 TPGICGPGTCYNTVGNYTCICPPDYMQVNGGNNCMAEYQALCSSG-PGMTSAGTDI 1710	Db 1656	
15 QQGLMSQVLRYHVVGCQQLLLDNLKVTTSATTLQGEPVSISVSQDTVFIN 564	Qy 51	
98 RPNPITVILEDIDECQELPGLCQGGKCINTFGSFQCRCPTGYYLNEDTRVCDDVNECE 1655	Db 159	
77FFQLQEHAVRELAGPGPFTVFAPLSSSFNHEPRIKDWD 514	Qy 47	
88 LDIRPRGDNGDTACSNEIGVGVSKASCCCSLGKAWGTPCELCPSVNTSEYKILCPGGEGF 1597	Db 1538	
65 476	ОУ 46	
34 GGNCTDVNECLDPTTCISGNCVNTPGSYTCDCPPDFELNPTRVGCVDTCSGNCY 1537	Db 1484	
YTEQDQRICTCKPDYTGDGIVCRG	Qy 45	

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R Interpro; IPR0001561; EGF-1ike.

R Interpro; IPR000742; EGF_2.

R Interpro; IPR001881; EGF_Ca.

R Interpro; IPR001881; EGF_Ca.

R Interpro; IPR001881; EGF_Ca.

R Interpro; IPR001491; Thrmbomoduln.

R Interpro; IPR001491; Thrmbomoduln.

R Pfam; PF00008; EGF; 19.

R PRINTS; PR00907; THRMBOMODULN.

R PRINTS; SM001181; EGF; 19.

R PROSTTE; SM001019; EGF_CA; 18.

R PROSTTE; PS00100; ASX_HYDROXYL; 14.

R PROSTTE; PS00100; ASX_HYDROXYL; 14.

R PROSTTE; PS001186; EGF_1; UNKNOWN_1.

R PROSTTE; PS01186; EGF_2; 19.

R PROSTTE; PS01187; EGF_CA; 12.

R PROSTTE; PS01187; EGF_CA; 12.
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MEDLINE=21347414; PubMed=1145543;
Nakayama A., Satou Y., Satoh N.;
"Isolation and characterization of genes the Ciona intestinalis metamorphosis.";
Dev. Genes Evol. 211:184-189(2001).
EMBL; AB041857; BAB40596.1;
HSSP; P00742; 1HCG.
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O1-JUN-2001 (TrEMBLrel. 1
O1-DEC-2001 (TrEMBLrel. 1
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Eukaryota; Metazoa; Chordata; Urochordata;
Cionidae; Ciona.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACWLASLAHNAKPAPGEVKMCA------LGTASVWDGVNGTGTCQCGLGFNG-----
                                                               LSSSFNHEPRIKDWDQQGLMSQVLRYHVVGCQQLLLDNLKVTTSATTLQGEPVSISVSQD
                                                                                                                         EC--RSSPCGNNAQCINT-PGSFTCRCNTGYTGNGRICRDVNECAAIRPPCSPNADCTNT
                                                                                                                                                                                                                                                                                                                                                                                               CKPGYRAQGSRCVDINECLRPN-VCGPASHNKRCVNTPGSFRCVCRNGYRAQGSRCVDIN
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Rhabditidae; Peloderinae; Caenorhabditi NCBI Tavid=6030:	00
<pre>caenornaboitis elegans. Eukaryota; Metazoa; Nematoda;</pre>	00
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01-DEC-2001 (TREMBLIE). 19, Last annotation upda Y64G10A.7 PROTEIN.	00
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VNYRPVCTCKPG	ם
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Db 718 CNRGYTGNGRVCFPVNPCSPSPCGSNAI 745	D.
WLESGRVAYPTTYAS-QKCG	Q
Db 693 NEC-NNPRACHPQATCANTP-GSYTCN 717	D.
RCLQDNGQCHPDASC	Ø
Db 639 IGYRKVRGNCVDINECR-ASRRPCDLNASCQNT-PGSFTCTCNTGYTGNGLTCADI 692	D
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PNADCTNTPGSFTCQCKPGYTGNGLVCRDINECSRPN-ACPRNQRCINTPGGF	D.
SVHATCTENNTCVCNLNYEGDGITCTVVDFCKQNNGGCA	Q
T-0	Ð
DEGITGSGECLCETGWTAASCDTPTAVFAVC	0
Db 514TCRCNTGYTGNGLICRDINECEAH 537	D.
RDLYTPMGQCLC	O
Db 486 GSRCVDIN	D.
MNPTLGGRCDTFTTFDIPGECGSCIFTPKCPLKSKPKC	Ö
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Qy 680 IRDSKALASDLPRSASWKTLQGSELSVRCGTGSDIGELFLNEQWCRFIHRGLLFDVGVAY 739	,O
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Matches 305; Conserv
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EMBL: AL110498; CAB60454.1; JOINED.
EMBL: AL110498; CAB57911.1; -.
EMBL: AL117206; CAB57911.1; JOINED.
HSSP: P00736; 1APQ.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR002049; Laminin_EGF.
Pfan: PF00008; EGF; 25.
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SMART; SM000179; EGF_CA; 4.

SMART; SM00001; EGF_11ke; 18.

PROSITE; PS00010; ASX_HYDROXYL; 4.

PROSITE; PS00122; EGF_1; UNKNOWN_22.

PROSITE; PS01186; EGF_2; 24.

PROSITE; PS01187; EGF_CA; 3.

Calcium-binding; EGF-11ke domain; Glycoprotein; Hydroxylation; Repeat.

SEQUENCE 1664 AA; 179279 MW; A69F093B4C705832 CRC64;
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544 VFGRRRHVKACVNFQGTLSLELFSSEVRTD----PSEKCPNGF----
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                                                                                                                                                                                                                                                                             381 CHENNG-----DCSQICVNLAGSVECQCKPGFRLMKDRKTCEDISECSSNNGGCE--QI 432
                                                                                                                                                                                                                                                                                                              381 CLENHGGCDRNAECTQTGPNQA---VCNCLP--KYTGDGKVCSLINVCLTNNGGCSPFAF
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                                                                                                                                                                                                                              CNYTEQDQRICTCKPDY--TGDGIVCRGSIYGELPKNPSTSQYFFQLQEHAVRE-LAGPG 492
                                                                                                                                                                                                                                                                                                                                                 YQLGRDGRTCEEMLGGCQVGNGGC--QHDCYDQPDGGHVCKCRNGYILANDQKLCHDINE
                                                                                                                                                                                                                                                                                                                                                                       FR--GNGTVC-TAINACETSNGGCSTKADCKRTTPGNRVCVCKAGY--TGDGIVCLEINP
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SQGPLGDGSCDCDVGWRGVKCDME--ITTDNC---NGTCHTSANCLLDPDGKASCKCAAG 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LHNGMHRETMLGFSYLLAFFLRNDQLYVNEAPINYTN-----VATDKGVIHGLEK 128
                                VAANHGYTKFSKLIQDSGLLSVITDSIHTPVTVFWPTDKALEALPPEQQDFLFNQDNKDK 670
                                                                   LAHDEKSCVAASDSADIFSNDIEDYSKVPGLDSIDEVIS--SIESYPADESPRPL----
                                                                                                                                                                       PFTVFAPLSSSFNHEPRIKDWDQQGLMSQVLRYHVVGCQQLLLDNLKVTTSATTLQGEPV 552
                                                                                                                                                                                                                                                                                                                                                                                                                      -----AQCQCYPGFH-LSYDRRSCVDIDECAKNNGCEHFCENV----KGTYRCKCREG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RTCGSGFHF--ENLILIKKVTSCSTDNGGCEHEC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RKCIYSIYEMGKRSVFI-------GCQPQCVRTIITRACWLASLAHNAKPAPGEVK 217
                                                                                                  SISVSQDTVFINNEAKVLSSDIISTNGV--IHVIDKLLSPKNLLITPKDALGRVLQNLTT 610
                                                                                                                                      CS-NQEGGYMCSCEPGFELSEDGHSC-----------HDMNECLINNG 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MCALGTASVWDGVNGTGTCQCGLGF----NGTAC---ETCTEGKYGIHCDQACSCVHGRC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142; Mismatches 451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 536; DB 5;
Pred. No. 8.1e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --ENDSNGEFY 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                      322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           274
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of rat fibrillin-2 cDNA and its role in branching nesis of embryonic lung."; 1. 212:229-242(1999).	ing of ra ogenesis Biol. 212	R 목 목
.S.;	. Y.S.;	RA
FROM N.A. 9350021 Fubbled=10419698; Ota K Tipubled=10419698;	CE FRC E=9935	RP RX
orvegicus (kat). a; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; ; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. ID-10116;	yota; M lia; Eu laxID=1	Z 2 2 2 2 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
	FIBRILLIN-2.	
999 (TrEMBLrel. 12, Created) 999 (TrEMBLrel. 12, Last sequence update) 001 (TrEMBLrel. 19, Last annotation update)	1999 1999 2001	DT DT
PRELIMINARY; PRT; 2906 AA.	Q9WUH9; Р	AC ID
	ILT 10 H9	RESUL Q9WUH
ALCDPISGHCS 1230	CDP	Db
FSC	AGYVGDO	Qy
ECLPGWSGEHCEKSCVSG	ന –	Db
SAGWLESGRVAYPTTYASOKCGANVVGIVDYGSRANK	1105 KYHLCSAGW	Qy
DCECIDGWTGPSCEFLCPFGQFGRNCAQRCNCF	E -	DЪ
FQDTTVGVFHLRSPLGQYKLTFDKAKEACAKEAATIATYNQLSYAQ	DASC	Qy
CRHSCQCSNGASCDRVTGFCDCPSGFMGKNCESECPEGLMGSNCMKHCLCMHGGECN 1137	1078 GEGCRHSCQ	ДĎ
KSHYVGDGVDCE-PEQLPLDRCLQDNGQC	1 1 1	Qy
RFGE	PDGRFG	рb
VNG-GCHMTGPG	GVNG-	Qy
	966 GKKGHKCDE	DЬ
ITCTVVDFCKQNNGGCAKVAKCSQKGTQV	937 NYEGDGI	Qy
SCECAPGWSGKKCDKACAPGTFGKDC	Ε	Db
ECLCETGWTAASCDTPTAVFAVCTPACSVHATCTENNTC	- 51	Qy
HTCSCVNGAKCDESDGSCHCTPGFYGATCSEVCPTGRFGIDCMQLCKCQNGAICD 912	SC	Db
FNGTAC-ELCWHGRFG	849	Qy
CPAGYFGYDCEQKCSCADVASPHKSKVCHHVTGTCTCLPGKTGPLCDQSCAPNTYGP 854	AGY	Db
NNRGMCRDLY		Qy
-RCKPGYYGHHCKRMCSPGLFGAGCAMKCSCPAGIRCDPVTGDCTKKCPAGYQGNLC 794	RC -	Db
PRCCHGYEMPDCQ	\circ	Qy
RCDPVFGYCTCPDGLYGQSCEKPCPHFTFGKNCRFPCKCARENSEGCDEITGKC 738	P۷	Db
FRRNVEGCQN	i	Qy
SDGPCPD	-VDC	Db
FDVGVAYGIDCLLMNPTLGG-RCDTFTTFDIPGECGSCIFTPK	<	Qy
: :	83	Db
E201 E26 E4 FACOZACAGOCERAGAGAZ EEGGGGEGGAACAGOCERGGGEFFACAGCAGEGAGAGAACAG	O / L LESSEEREHV	VΩ

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Qγ
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Best Local Similarity
Matches 301; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO0010; EGFBLOOD.

SMART; SM00179; EGF_CA; 42.

SMART; SM00001; EGF_LIKe; 4.

PROSITE; PS00070; ALDEMYDE_DEHYDR_CYS; UNKNOWN_1.

PROSITE; PS00010; ASX_HYDROXYL; 43.

PROSITE; PS00022; EGF_1; UNKNOWN_2.

PROSITE; PS01186; EGF_2; 36.

PROSITE; PS01186; EGF_CA; 43.

Calcium-binding; EGF-Like domain; Glycoprotein; Hydroxylation; SEQUENCE 2906 AA; 313371 MW; 9EE64E727044EF58 CRC64;
 1076
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HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002086; Aldehyde_dehydr.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000161; EgF-like.
InterPro; IPR001881; EgF_Ca.
InterPro; IPR001438; EgF_II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam;
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                                                                                                                                                                                         924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QCVRTIITRACWLASLAHNAKPAPG---EVKMCALGTASVWDGVNGTGT--CQCGLGFNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DGENCVGHDECTTINMCLNGMCINEDGSFKCVCKPGFVLAPNGRCCTDVDECQTPGICMN
 CTYGKCRNTI--GSFKCRCNSGFALDMEERNCTDIDECRISPDLC--
                                                                                                                                                                                         -- CERCELD-----
                                                                                                                                                                                                                                                                                                                                         DGKVCSLINVCLTN---NGGCSPFAFCNYTEQDQRICTCKP--DYTGDGIVCRGSIYGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCANPDYGFGEPCQPCPAKNSAEFHGLCSGGVGITVDGRDINECALDPDICANGICENL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GHCINNEGSFRCDC---PPGLAVGVDGRVCVDTHMRSTCYGEIKKGVCVRPFPGAVTKYE 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D--NCNG--TCHTSANCL----LDPDGKASCKCAAGF--RGNGTVCTAINACET----SN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T----ACETCTEGKYGIHCDQ-ACSCVHGRCSQGPLGDGS--CDCDVGWRGVKCDMEITT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RCIPTVSSYRC-ECNMGYK-QDANGDCIDVDECTSNPCSHGDCVNTPGSYYCKCHAGFQR
                                                              CAVGAAWGTECEECPKPGTKEYETLCPRGPGF---ANRGDILTGRPFYKDINECKALPGM
                                                                                               TPVTVFWPTD----
                                                                                                                                                      VIDKLLSPKNLLITPKDALGRVLQNLTTVAANHGYTKFSKLIQDSGLLSV----ITDSIH
                                                                                                                                                                                                                     VGCQQLLLDNLKVTTSATTLQGEPVSISVSQDTVFINNEAKVL-----SSDIISTNGVIH
                                                                                                                                                                                                                                                     WLNIQDNRCEVNINGATLKS----
                                                                                                                                                                                                                                                                                   PKNPSTSQYFFQLQEHAVRELAGPGPFTVFAPLSSSFNHEPRIKDWDQQGLMSQVLRYHV
                                                                                                                                                                                                                                                                                                                 ETETCEDVNECESNPCVNGACR-----NNLGSFHCECSPGSKLSSTGLICIGSLKGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPTKQACIDIDE - - - - - CIQNGVLCKNGRCVN - - - TDGSFQCICNAGF - - - - - - ELTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF135060;
P35555; 1
                                LPRSASWKTLQGSELSVRCGTG------
                                                                                                                                                                                                                                                                                                                                                                                RGSYRCNCNSGYEPDASGRNCIDIDECLVNRLLCD-NGLCRNT-PGSYSCTCPPGYVFRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00008; EGF; 46. PF00683; TB; 9.
                                                                                                                          -CECPEGLTL---DGTGRVCLD---VRMEHCFLKWD---EDECVHPVPGKFRMDACC
                                                                                                                                                                                                                                                                                                                                                                                                           -CKAGYTGD--GIVCLEINPCLENHGGCDRNAECTQTGPNQAVCNCLPKYT--G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STKADCKRTTPG-----NRVCV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD34439.1;
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                                                                                          ----KALEALPPEQQDFLFNQDNKDKLKSYLKFHVIRDSKALASD
                                                                                                                                                                                       -AACPRGFARIKGVTCEDV---NECEVFPGVCPNGRCVNNKGSFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 519.5; DB 11;
Pred. No. 4.9e-34;
24; Mismatches 407;
                                                                                                                                                                                                                                                     ECCATLGTA-----
                  SDIGELFLNEQMCRFIHRGLLFDVGVAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
-GNGICVNTPGSF
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RESULT
Q25253
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                                                                                                                                                                                                                                                                                                                                                                                                                          Q25253
Q25253;
Q1-NOV-1996
Q1-NOV-1996
Q1-DEC-2001
                                                                                                       STRAIN-SS
Chen Z., N
                                                                                                                                                                             Davies A.G., Game A.Y., Chen Z., Williams T.J., Goodall S., McKenzle J.A., Batterham P.;
"Scalloped wings is the Lucilia cuprina Notch homologue and candidate for the modifier of fitness and asymmetry of diazi resistance.";
Chen Z., McKenzie J.A., Batterham P.; Submitted (NOV-1997) to the EMBL/GenEEMBL; U58977; AAC36151.1; -.
                                            STRAIN=SS
                                                                                                                                    [2]
SEQUENCE OF 39-265
                                                                                                                                                                                                                                                        STRAIN=SS SEEKING;
MEDLINE=96400928;
                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=7375;
                                                                                                                                                                                                                                                                                                                                 Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Lucilia.
                                                                                                                                                                                                                                                                                                                                                                                                            NOTCH HOMOLOG SCALLOPED WINGS (SCL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1557
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                                                           [3]
SEQUENCE OF 39-265 FROM
                                                                                                                                                                   Genetics
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GANVVGIVDYGSRANKSEMWDVFCYRMK-----DVNCTCKAGYVGDGFSCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {\tt NGQCLNVPGAYRCECEMGFTPASDSRSCQDIDECSFQNICVFGTCNNLPGMFHCICDDG-}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLDECANGTH-QCSINAQCVNT-PGSYRCACSEGFTGDGFTCS----DVDECAENINLCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EIDPCADGVNGGCHEHATCRWTGPGKHKCECKSHYVGDGVDCEPEQLPLDRC-----LQD 1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIC-DGGQC-TNIPGEYRCLCYDGF-MASMDMKTCIDVNECDLNPNICMFGEC-ENTKGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KSKPKGVKKKCI-YNPLPFRRNVEGCQN-LCTVVIQTPRC-CH-GY-FMPDCQACP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ECECFEGYESGFMMMKNCMDIDECERNPLLCRGGTCVNTEGSF----QC-----DCPL 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NATGVGCVD - - NRVGN - - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YGL -- DRTGGHCTDIDECADPINCVNGLCVNTPGRYE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YKLTFDKAKEACA---KEAATIATYNQLSYAQKAKYHLCSAGWLESGRVAYPTTYASQKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGQC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FICHCQLGYSVKKGATGCTDVDECEIGAHNCDMHASCLNVPGSFKCSCREGWVGNGIKCI 1399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RSCSEHGQCDEGITGSGECLCETGWTAASCDTPTAV-FAVC--TPACSVHATCTENN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CMIMNGGCDTQCTN---SEGSY----ECSCSEGYALMPDGRSCADIDEC----ENNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -TCVCNLNYE-GDGIT-CTVVDFCKQNNGGCAKVAKCSQKGTQVSCSCKKGYKGDGYSCI
                                                                                                      Newsome
                                                                                        Newsome T.,
1 (DEC-1997)
                                                                                                                                                                  143:1321-1337(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -GGPDTPCNNRGMCRDLYTPMGQCLCHTGF----NGTAC---ELCWHGRFGPDCQP 876
                                             SEEKING;
                                                                                                                      SEEKING;
                                                                                                                                                                                                                                                                                                                                                                                                                          (TrembLrel. 01, Created)
(TrembLrel. 01, Last sequence united (TrembLrel. 19, Last annotation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                          PubMed=8807304;
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to the EM
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                                                                                         ie J.A., Batterham
EMBL/GenBank/DDBJ
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                                                                                                      J.A.,
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Best Local Similarity
Matches 298; Conserv
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Pfam; PF00008; EGF; 36.

Pfam; PF00066; notch; 3.

PRINTS; PR00010; EGFBLOOD.

PRINTS; PR001010; EGFBLOOD.

PRINTS; PR0011452; NOTCH.

SMART; SM002148; ANK; 4.

SMART; SM00001; EGF_like; 11.

SMART; SM00001; EGF_like; 11.

SMART; SM000088; ANK_REPEAT; 5.

PROSITE; PS50088; ANK_REP_REGION; 1.

PROSITE; PS00010; ASX_HYDROXYL; 22.

PROSITE; PS00022; EGF_1; UNKNOWN_34.

PROSITE; PS01186; EGF_2; 28.

PROSITE; PS01187; EGF_CA; 21.

ANK repeat; Calcium-binding; EGF-like do:
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                                                                                          AVCNCLPKYTGDGKVCSL-INVCLT----NNGGCSPFAFCNYTEQDQRICTCKPDYTGDG
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IISTNGVIHVIDKLLSPKNLLITPKDALGRVLQNLTTVAANHGYTKFSKLIQDSGLLSVI
                                                  QGLMSQVLRY--HVVGCQQLLLDNLKVTTSATTLQGEPVSISVSQDTVFINNEAKVLSSD
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P00740; 1EDM.
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IPR000742;
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                           -GKDCEINVNE - -
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development.";
Am. J. Physiol.
[2]
                                                             SEQUENCE FROM N.A. MEDLINE=99032689; Kanwar Y.S., Ota K
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             275:F710-F723(1998)
                                                             PubMed=9815129;
K., Yang Q., Kum
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Best Local Similarity
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Pfam; PF00008; EGF; 45.

Pfam; PF00008; EGF; 45.

SMARR; SM0179; EGF_CA; 41.

SMARR; SM0179; EGF_Like; 5.

PROSITE; PS00010; ASX_HYDROXYL; 42.

PROSITE; PS00010; EGF_1; UNKNOWN_2.

PROSITE; PS01186; EGF_2; 38.

PROSITE; PS01186; EGF_2; 38.

PROSITE; PS01187; EGF_CA; 41.

PROSITE; PS01087; EGF_CA; 41.

PROSIT
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InterPro; IPR000561; I
InterPro; IPR001881; I
InterPro; IPR002212; I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Kanwar Y.S.;
                                              649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DYTGD--GIVCRGSIYGELPKNPSTSQYFFQLQEHAVRELAGPGPFTVFAPLSSSFNHEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PNQAVCNCLPK---YTGDGKVCSLINVCLTN---NGGC--SPFAFCNYTEQDQRICTCKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GECINNQGSYTCHCRAGYQSTL--TRTECRDIDECLQNGRICNNGRCIN---TDGSFHCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WDGVNGTG--TCQCGLGFNGTACETCTEGKYGIHCDQ-ACSCVHGRCSQGPLGDGS--CD
                                                                                                                                                                                                   KDALGRVLQNLTTVAANHGYTKFSKLIQDSGLLSVI----TDSIHTPVTVFWPTD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIKDWDQQGLMSQVLRYHVVGCQQLLLD-NLKVTTSATTLQ------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CALDPDICPNGICENLRGTYKCICNSGYEVDITGKNCVDINECVLNSLLCD-NGQCRNT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RGQCVKPLFGAVTKSECCCASTEYAFGEACQPCPAQNSAEYQALCSSGPGMTSAGSDINE
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                                                                                                                      -DATGRICLDIRL-----ETCFLKYDDEECTLPIAGRHRMDACCSSVGAAWGTEECEEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESTLDPTKTICIETIKGT - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGRYCKDINECETPGICMNGRCVNTDGSYRCECFPGLAVGLDGRVCVDTHMRSTCYGGYR
                                          KALEALPPEQQDFLFNQDNKDKLKSYLKFHVIRDSKALASDLPRSASWKTLQGSE
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                                                                                                                                                                                                                                                                                                                                                                -SVSQDTVFINNEAKVLSSDIISTNGVI---HVIDKLLSPKNLLITP
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EGF-like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    -CWQTVIDGRCEININGATLKSECCSSLGAAWGSPCTICQ
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Pred. No. 2.4e-32;
Pred. No. 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ
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                  MGD; MGI:97364; Notch2.

InterPro; IPR002110; ANK.

InterPro; IPR000152; Asx.hydroxyl.

InterPro; IPR000561; EGF-like.

InterPro; IPR000742; EGF_2.

InterPro; IPR001881; EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                     035516;
01-JAN-1998
01-JAN-1998
01-DEC-2001
                                                                                                    single copy of mouse Notch2 gene.";
Submitted (JUI-1994) to the EMBL/GenBank/DDBJ
EMBL; D32210; BA322094.1; -
HSSP; P16109; 1FSB.
                                                                                                                                                                                                                     Lardelli M., Lendahl U.;
"Motth A and Motth B - two mouse
wide variety of tissues.";
Exp. Cell Res. 204:364-372(1993)
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=C57B/6; TISSUE=THYMUS;
MEDLINE=93178563; PubMed=8440332;
                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         035516
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                                                                                                                                                     SEQUENCE FROM N.A.
STRALN=C57B/6; TISUE=THYMUS;
Hamada Y., Higuchi M., Tsujimoto Y.;
"Complete amino acid sequence and mutliform transcripts
                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
[1]
                                                                                                                                                                                                                                                                                                                                                                               NOTCH2
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              InterPro;
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iPR001881;
iPR001438;
iPR000800;
                                                                                                                                                                                                                                                                                                                                                                                                    8 (TrEMBLrel. 05,
8 (TrEMBLrel. 05,
1 (TrEMBLrel. 19,
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                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN
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 EGF_II.
                                                                                                                                                                                                                                               two mouse
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                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                  Notch
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Murinae; Mus
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Best Local S
Matches 282
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SMART; SM00179; EGF_CA; 22.

SMART; SM00001; EGF_11ke; 12.

SMART; SM00004; NL; 3.

SMART; SM00004; NL; 3.

PROSITE: PS50088; ANK_REP_REGION; 1.

PROSITE: PS50097; ANK_REP_REGION; 1.

PROSITE: PS00010; ASX_HYDROXYL; 22.

PROSITE: PS001187; EGF_1; UNKNOWN_33.

PROSITE: PS01187; EGF_CA; 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00023; ank; 6.
Pfam; PF00008; EGF; 32.
Pfam; PF00066; notch; 2.
PRINTS; PR00010; EGFBLOOD.
PRINTS; PR01452; NOTCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANK repeat; Calcium-binding; EGF-like Hydroxylation; Repeat. SEQUENCE 2470 AA; 265325 MW; B55A3
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                                                                                                              SDLPRSASWKTLQGSELSVRCGTGSDIGELFLNEQMCRFIHRGLLFDVGVAYGIDCLLMN
                                                                                                                                            GWVGVNCE-
                                                                                                                                                                     GLLSVITDSIHTPVTVFWPTDKALEALPPEQQDFLFNQDNKDKLKSYLKFHVIRDSKALA
                                                                                                                                                                                                   RKGATCINDVNGFRCICPEGPHHPSCYSQVNECLSNPCIHGNCTGGLSGY - - -
                                                                                                                                                                                                                        KVLSSDIISTNGVIHVIDKLLSPKNLLITPKDALGRVLQNLTTVAANHGYTKFSKLIQDS
                                                                                                                                                                                                                                                                                    WDQQGLMSQVL-----RYHVVGCQQLLLDNLKVTTSATTLQGEPVSISVSQDTVFINNEA
                                                                                                                                                                                                                                                                                                                \verb|M--GAICSDQI-DECYSSPC-----LNDGRCIDLVN-GYQCNCQPGTSGLNCEINFDD||
                                                                                                                                                                                                                                                                                                                                             TGDGIVCRGSIYGELPKNPSTSQYFFQLQEHAVRELAGPGPFTVFAPLSSSFNHEPRIKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                               GYAGPRCEMDI -- NECHSDPCQNDATC - LDKIGGFTCLCMPGFK -- GVHCELEVNECQSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GWRGVKCDMEITTDNCNG-TCHTSANCLLDPDGKASCKCAAGFRGNGTVC-TAINACET-
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 -KGV-
                          PYTGKNCQTVLAPCSPNPCENAAVCKEAPNFESFSCLCAPGWQGKRCTVDVDECISKPCM
                                                        PTLGGRCDTFTTFDIPGECG:
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                                                                                                                                          -----VDKNECLSNPCQNGGTCN----NLVNGY--
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22.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 489; DB 11;
Pred. No. 1.5e-31;
9; Mismatches 445;
                                                                                                                                                                                                                                                                                                                                                                          ILCDENIDNCDPDP-CHHGQCQDGIDSYTCICNPGY
                                                                                   NIDECASNP - - C - - LNQGTCFDDVSGYTCHCML - -
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KKKCIYNPLPFRRNVEGCQN--LCTVVIQTPR
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                                                        SCIFTP---
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                                                     --KCPLK-
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096PA5

096PA5;

1 01-MAR-2001 (TrEMBLrel. 16,
JT 01-DEC-2001 (TrEMBLrel. 19)

DT 01-DEC 2001 (TREMBLREL 19)

"""ATIVE NOTCH RECEPTOR PF
                                                               InterPro; IPR002110; ANK.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR000742; EGF_2.
InterPro; IPR0001881; EGF_Ca.
InterPro; IPR0001438; EGF_II.
InterPro; IPR0002049; Laminin_EGF.
InterPro; IPR000800; Notch.
                                                                                                                                                                           Notch (AmphiNotch): evolutionary conservation domains in amphioxus and vertebrates."; Submitted (APR-2000) to the EMBL/GenBank/DDBJ EMBL; Y12539; CAC19873.1; -. HSSP; P00740; LEDM.
                                                                                                                                                                                                                                              Holland L.Z., Burgtorf C., Holland N.D., Lehn Abi-Rached L., Pontarotti P., Lardelli M.; "Cloning and developmental expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1242
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                                      Pfam; PF00008; EGF; 36. Pfam; PF00066; notch; 3
                                                                                                                                                                                                                                                                                           TISSUE=LARVA;
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                      Branchiostoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HCETFLDVCPQKPCLNGGTCAVASNMPDGFICRCPPGFSGARLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIGGYTCRCLPGFAGERCEGDINECL---SNPCSSE-GSLDCVQLKNNYNCICRSAFTGR
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          PR00010;
PR00011;
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tazoa; Chordata;
        EGFBLOOD.
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                                                                                                                                                                                                                                                                                                                                                                (Florida lancelet) (Amp)
ordata; Cephalochordata;
                                                                                                                                                                                                                                                                                                                                                                                                         . 16, Created)
. 16, Last sequence upo
. 19, Last annotation of R PROTEIN.
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                                                                                                                                                                                                                                                                              Lehrach H.,
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Best Local S
Matches 271
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SMART; SM00111; EGF; 37.
SMART; SM001179; EGF_CA; 34.
SMART; SM00001; EGF_11ke;
SMART; SM00004; NL; 3.
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 918
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Local Similarity 22.1%; Pr
hes 271; Conservative 107;
                                                                                                                                                                                                                                                                                           GYEGNNCEREIDECASSPCHNGGI --
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{\tt YT----CSCMPGFGGTNCEEDIDECYSNPCQNGGQCIDAVNGYACDCVVGFIGTNCQTNK}
                              YTPMGQCLCHTGFNGTACEL ---
                                                                                     NVEGCONLCTVVIQTPRCCHGYFMPDC-----
                                                                                                                                                TFTTFDIPGEC --
                                                                                                                                                                           CQCLPGYE-GVNCDINTD--ECASNP--CQ--NGGRCLDGVNNYVCDCDL--PFVGTNCQ
                                                                                                                                                                                                       WKTLQGSELSVRCGTGSDIGELFLNEQMCRFIHRGLLFDVGVAYGIDCLLMNPTLGGRCD
                                                                                                                                                                                                                                  VNECESSPCAHGTCQDGINDYTCTCENGYEGKNCDVNIDECASNPCQHEGQCDDGIGRYE
                                                                                                                                                                                                                                                                DN---
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                                                                                                                                                                                                                                                                                                                                                                                                         TYACTCLEGFTGTDCEINIDDCQSNQCQHGTCVDGVASFTCSCEPGYNGPLCESPVDECD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PNICLNCGTCHNTVGGYSCVCVNGWIGDDCSENF - - DDCASAACFDGATC - HDRVGFFMC
                                                            NGAPCVNL--
                                                                                                                  TELAPCRPNPCENLGACIPSADYQTFTCNC----ADGFEGETCADDINECQSNPC---K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -EHAVRELAGPGPFTVFAPLSSSFNHEPRIKDWDQQGLMSQVLRYHVVGCQQLLLDNLKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - IDDIGEFRCACMPGFAGD--LCETDV-DECASSPCLNGLCRDGINKYECECDPGFEGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2524 AA; 270969 MW;
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                                                                                                                                              -GSCI----FTPKCPLKSKPKGVK-----KKCIYNPLPFRR
                                                                                                                                                                                                                                                               KDKLKSY-LKFHVIRDSKALASDLPRSAS-----
                                                                                                                                                                                                                                                                                                                      FSKLIQDSGLLSVITDSIHTPVTVFWPTDKALEALPPEQQDFLFNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                     -EPVSISVSQDTVFINNEAKVLSSDIISTNGVI--HVIDKL-
                                                          *EGDFRCDCLMGFAGELCSVNIDDCDPDPCHNGGTCNDGINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 486.5; DB 5;
Pred. No. 2.5e-31;
17; Mismatches 413;
                                                                                                                                                                                                                                                                                                                                                                              -LSPKNLLITPKDALGRVL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C2CA57E306D23EC9 CRC64;
                                                                                                                                                                                                                                                                                           -CHDLVNAF - - - - SCECPPGYHDQLCYSN
                                                                                     -QACPGGPD----TPCNNRGMCRD---L
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                              -CWHGRFGPDCQPR-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----DLVT
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RESULT
Q9XWD6
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., MortLnore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen I
smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-DEC-2001 (TrEMBLrel. 19, Y47H9C.4 PROTEIN (CED-1). Y47H9C.4 OR CED-1.
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           Cell 104:43-56(2001).
EMBL; AL032657; CAA21739.1;
EMBL; AF332568; AAG60061.1;
InterPro; IPR000561; EGF-11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans
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                                                                           "CED-1 is a Transmembrane Re
Engulfment in C. elegans.";
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                                                                                                        MEDLINE=21097720;
                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                          Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                            Harris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VGVFHLRSPLGQYKLTFDKAKEACAKEAATIATYNQLSYAQKAKYH--LCSAGWLESGRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NGAECR-DGLGTYTCACRPGY--QGVNCEQE---INECI--SNPCQNGGTCIDM-----
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                                                                                                                                                                          368:32-38(1994).
                                                                                                          21097720; PubMed=11163239; Hartwieg E., Horvitz H.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FROM N.A.
IPR002174;
                                                                                                                                                                                                                                                                                                                                                                                                                            (OCT-1998) to
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              EGF-like
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhabditida; Rhabditoidea;
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Best Local Similarity 22.2
Matches 251; Conservative
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SMART; SM0001; EGF_like; 5.

SMART; SM00261; Fig. 2.

PROSITE; PS00022; EGF_1; UNKNOWN_15.

PROSITE; PS01186; EGF_2; 11.

EGF-like domain; Glycoprotein.

EGF-like domain; Glycoprotein.

SEQUENCE 1111 AA; 118803 MW; A39F374C008F9874 CRC64;
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 834
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                                                                                                                                                                                                                                                                                                                                                                            GPFTVFAPLSSSFNHEPRIKDWDQQGLMSQVLRYHVVGCQQLLLDNLKVTTSATTLQGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QNGGKCNK----EGKCVCSDGWGGEFCLNKCEEGKFGAECKFE-----CN--CQNGATC- 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEKYVKQCCDGYYQTKDHFCLPDCNPPCKKGKCIEPGKC-----ECDPGYGG-KYCAS
                                                                                                                         LLFDVGV---AYGIDCLLMNPTLGGRCDTFTTFDIPGECGSC---IFTPKCPLK-SKPKG
                                                                                                                                                                                                                                                                                                                                                CPLDFYGP---NCAHQCQC---NQRG-----VGCD-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YGADCSKTCTCVRENTLMCAPNTGFCRCKPGFYGDN--CEL--ACSKDSYGPNCEKQAMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HGG-CDRNAECTQ-----TGPNQAVCNCLPKYTGDGKVCSLINVCLTNNGG--CSPFAEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --GCST---KADCKR--TTPG------NRVCVCKAGYTGDGIVCLEINPCLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNTNGKCICKSGYHGALCENECSVGFFGSGCTQKCDCLNNQNCDSSSGECKCIGWTGKHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LDPDGKASCK-----CAAGFRGNGTV--CTAIN--ACETSNG-------
 PC--NNRG-MCRDLYTPM-----
                                                           VKKKCIYNPLPFRRNVEGCQNLC-----TVVIQTPRCCHGYFMPDCQACPGGP-----DT
                                                                                        ANCDIGCPEGSYGPGCKLHCKCVNGKCDKET-----GEC-TCQPGFFGSDCSTTCSKGK-
                                                                                                                                                                                      KSYLKFHVIRDSKALASDLPRSASWKTLQGSELSVRCGTGSDIG-ELFLNEQMCRFIHRG
                                                                                                                                                                                                                                                   AANHGYTKFSKLIODSGLLSVITDSIHTPVTVFWPTDKALEALPPEQQDFLFNQDNKDKL
                                                                                                                                                                                                                                                                                                                 VSISVSQDTVFINNEAKVLSSDIISTNGVIHVIDKLLSPKNLLITPKDALGRVLQNLTTV
                                                                                                                                                                                                                                                                                                                                                                                                               DWNHASECNPETGSCVCKPGRTG--
                                                                                                                                                                                                                                                                                                                                                                                                                                            NYTEQDQ-----RICTCKPDYTGDGIVCRGSIYGELPKNPSTSQYFFQLQEHAVRELAGP 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIGCSRGRFGLQCKQNCTCPGLEFSDSNASCDAKTGQCQCESGYKGP--KCDERKCDAEQ
                               -----YG-----ESCELSCPCSDASCSKQTGKC------LCPLGTKGVSCDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.1%;
22.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 480.5; DB 5;
; Pred. No. 2.2e-31;
98; Mismatches 341;
                                                                                                                                                                                                                       HCPADTF ----
                                                                                                                                                       ---GANCEKRCKCPKGIGCDPITGECTCPAGLQG
-GQCL-CHTGFNGTACE-LCWHGRFGPDCQP-RS
                                                                                                                                                                                                                                                                                                                                                                                                               ----KNCSE--
                                                                                                                                                                                                                                                                                  --GADGKCQCDRGWTGH
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                                          1030 EPEQLPLDRCLQDNGQCHPDASCADLYFQDTTVGVFHL-RSPLGQYKLTFD
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                                                                                                              IEIDPCADGVNG-GCHEHATCRWTGPG-----KHKCECKSHYVGD-------GVDC 1029
                                                                                                                                                                                                                                                                                                                                                     KCDPNTFGFLCQETVTPSPCASTDPKNGVCLSCPPGSSGIHCEHNCPAGSYGDGCQQVCS
                                                                                                                                                                           CICPAGLE -- GALCTRPCSAGFWGNGCRQVCRCTSEYKQCNAQTGECSCPAGFQGD--RC
                                                                                                                                                                                                                      CVCNLNYEGDGITCTVVDFCKQNNGGCAKVAKCSQKGTQVS-----CSCKKGYKGDGYSC
                                                                                                                                                                                                                                                                 {\tt CADGHGCD---PTTGECICEPGYHGKTCSEKCPDGKYGYGCALDCPKCASGSTCDHINGL}
                                                                                        {\tt DK--PCEDGYYGPDCIKKCKCQGTATSSCNRVSGACHCHPGFTGEFCHALCPESTFGLKC}
                                                                                                                                                                                                                                                                                                            CSEHGQCDEGITGSGECLCETGWTAASCD--TPTAVF----AVCTPACSVHATCTE-NNT
-C-PKDGCGDGYECDAAIGCCHVDQMSCGKAKQEFE
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Search completed: June 17, 2002, 12:35:05 Job time: 321 sec

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